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OM protein - protein search, using sw model

Run on: October 17, 2004, 15:21:58 ; Search time 94 Seconds
(without alignments)
1118.167 Million cell updates/sec

Title: US-10-716-488-2

Perfect score: 1951

Sequence: 1 MSTAALITLVRSNGNQVRR.....KNSEINFSESFSSGRWA 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : A_Geneseq_29Jan04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1951	100.0	372	5	Aae23954 PN7740 pr
2	1951	100.0	372	5	Abb79999 Human pro
3	1951	100.0	372	5	Abg70789 Fe65 inte
4	1951	100.0	372	5	Aae23953 PN7740 pr
5	1951	100.0	372	5	Abg70801 Fe65 inte
6	1951	100.0	372	5	Abg70826 Fe65 inte
7	1951	100.0	372	5	Abb07402 Human pro
8	1951	100.0	372	5	Aae23976 Human PN7
9	1951	100.0	372	5	Aae24078 Human PN7
10	1951	100.0	372	5	Aae14451 Human pro
11	1951	100.0	372	6	Abu10309 Human pro
12	1951	100.0	372	6	Aac23055 Human ser
13	1951	100.0	372	7	Adb66824 Human PN7
14	1951	100.0	372	7	Adb73452 Novel hum
15	1950	99.9	372	6	Ada54131 Human pro
16	1939	99.4	373	4	Aau29334 Novel hum
17	1924	98.6	373	3	AAb57077 Human pro
18	1809	92.7	351	5	Abb07401 Human pro
19	1727	88.5	352	5	Abb78059 Amino aci
20	1727	88.5	352	7	Adb31687 Human 161
21	1538.5	78.9	373	5	Abb07392 Human pro
22	1375.5	70.5	1072	4	Abg06716 Novel hum
23	1375.5	70.5	1195	4	Abg28412 Novel hum
24	1150	58.9	238	4	Aam41604 Human pol
25	951.5	48.8	233	4	Aab47431 Human pro

ALIGNMENTS

RESULT 1
AAE23954 standard; protein; 372 AA.

AAE23954

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Aam39818 Human pol
Ada55670 Human pro
Abb07393 Human pro
Abb07397 Human pro
Aag66997 Arabidops
Aag98824 Arabidops
Aae01345 Arabidops
Abb07400 Amino aci
Aae04841 Human SGP
Aau75784 Human pro
Abb78060 Consensus
Abb07398 Human pro
Aae01349 Arabidops
Aag66998 Arabidops
Aag09825 Arabidops
Aag18039 Arabidops
Aag39774 Arabidops
Aag39776 Arabidops
Aag18041 Arabidops
Aag18040 Arabidops
Aag39775 Arabidops
Aag16902 Arabidops
Aae01344 Arabidops
Aae36344 Arabidops
Aae01348 Arabidops
Abb31924 Herbicida
Abr33510 Protein s
Abb31997 Herbicida
Abb32779 Herbicida
Aag16903 Arabidops
Aag43887 Arabidops
Abp72388 Rat prote
Ade61989 Rat Prote
Ade58683 Rat Prote
Ade61804 Rat Prote
Ade61808 Rat Prote
Ade61806 Rat Prote
Ade61810 Rat Prote
Abb92777 Herbicida
Abb91646 Herbicida
Abp72390 Rat prote
Aam38769 Human pol
Aab28791 Human hyd
Aab92585 Human pro
Abb05726 Human sig
Abg73740 Human ILK
Adb90823 Human hyd
Ade55462 Human Pro
Ade55454 Human Pro
Ade55466 Human Pro

Protein-protein interaction; neurodegenerative disorder; dementia;
Huntington's disease; Parkinson's disease; Alzheimer's disease; AD;
protein therapy; drug screening.

Unidentified.

WO200233114-A2.

PD 25-APR-2002.
 XX 16-OCT-2001; 2001WO-US032199.
 PF 17-OCT-2000; 2000US-0240790P.
 XX (MYRI-) MYRIAD GENETICS INC.
 XX
 XX Roch J, Bartel PL, Heichman K;
 XX WPI; 2002-454609/48.
 DR N-PSDB; AAD38600.
 DR
 XX
 XX New protein complexes involved in neurodegenerative diseases, useful for
 PT diagnosing the presence of or a predisposition to a neurodegenerative
 PT disorders (e.g. Alzheimer's) or in screening for drugs for treating the
 PT diseases.
 XX
 XX Example 6; Page 52; 93pp; English.
 PS
 XX The invention relates to the discovery of protein-protein interactions
 CC that are involved in the pathogenesis of neurodegenerative disorders,
 CC including Alzheimer's disease (AD). The invention is also directed to
 CC protein complexes involved in neurodegenerative disorders. The protein
 CC complexes are useful for diagnosing the presence of or a predisposition
 CC to neurodegenerative disorders (e.g. Huntington's disease, Parkinson's
 CC disease, dementia and Alzheimer's disease). They are also useful in drug
 CC screening. The invention is used in protein therapy. The present sequence
 CC is PN7740 protein. This sequence is used in the exemplification of the
 CC invention
 XX
 XX Sequence 372 AA;
 PS
 XX
 XX Query Match 100.0%; Score 1951; DB 5; Length 372;
 CC Best Local Similarity 100.0%; Pred. No. 1.5e-206;
 CC Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 QY 1 MSTAALITLVRSNGQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRFPDGGSPAT 60
 Db 1 MSTAALITLVRSNGQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRFPDGGSPAT 60
 QY 61 WDNFGIWNDRIDEPILLPPSIKYGKIPKISLENVGCASQIGKRENERDFPAQLTDEV 120
 Db 61 WDNFGIWNDRIDEPILLPPSIKYGKIPKISLENVGCASQIGKRENERDFPAQLTDEV 120
 QY 121 LYFAVDGHHGPPAAADPCHTHMEKIMDLLPKENLETLTLTFLAFLIDKAFSSHARLSAD 180
 Db 121 LYFAVDGHHGPPAAADPCHTHMEKIMDLLPKENLETLTLTFLAFLIDKAFSSHARLSAD 180
 QY 181 ATLLTSGTTATVALLRDGIELVWASGDSRAILCRGKPKMKLTIDTTPRKEKERIKKC 240
 Db 181 ATLLTSGTTATVALLRDGIELVWASGDSRAILCRGKPKMKLTIDTTPRKEKERIKKC 240
 QY 241 GGFVAMNSLGPHVNGFLAMTRISGDLDTKTSGVIAEPETKRIKLHADDLSFLVLTGDI 300
 Db 241 GGFVAMNSLGPHVNGFLAMTRISGDLDTKTSGVIAEPETKRIKLHADDLSFLVLTGDI 300
 QY 301 NFVNSQEIICDFVNOCHDPNEAAHVAITEQAIQYGTEDNSTAVVVPFGANGKYKNSINFS 360
 Db 301 NFVNSQEIICDFVNOCHDPNEAAHVAITEQAIQYGTEDNSTAVVVPFGANGKYKNSINFS 360
 QY 361 FSRSFASSGRWA 372
 Db 361 FSRSFASSGRWA 372
 RESULT 2
 ID ABB79999 standard; protein; 372 AA.
 XX ABB79999;
 XX ABB79999;
 XX 19-DEC-2002 (first entry)

XX Human phosphatase PN7740.
 DE PN7740; phosphatase; enzyme; human neurodegenerative disease;
 XX Alzheimer's disease; dementia; Parkinson's disease; Huntington's disease;
 KW diagnosis; therapy.
 KW Homo sapiens.
 OS
 PI Key Location/Qualifiers
 FH 104. .339
 FT Domain /note="phosphatase 2C domain"
 FT
 XX US2002115607-A1.
 PN 22-AUG-2002.
 XX 12-OCT-2001; 2001US-00975072.
 PD 17-OCT-2000; 2000US-0240790P.
 PF (MYRI-) MYRIAD GENETICS INC.
 PR Roch J, Bartel PL, Heichman K;
 XX WPI; 2002-722778/78.
 XX N-PSDB; ABQ81507.
 DR
 DR New protein complex useful for treating neurodegenerative disease e.g.
 XX Alzheimer's, comprises two proteins or their fragments, for e.g. BAT3
 PT with glypican, LRP2, LRPAP1 or transthyretin.
 PT
 XX Example 2-33; Page 23; 41pp; English.
 PS
 XX The present sequence is the protein sequence of a novel human
 CC phosphatase, designated PN7740. The sequence is predicted from a human
 CC brain cDNA clone identified in a yeast two-hybrid screening using as bait
 CC a fragment of F665 protein (amino acids 360-552, i.e. the first
 CC phosphotyrosine binding domain (PTB)). Identification of a phosphatase 2C
 CC domain showed PN7740 to be a novel phosphatase that binds to the first
 CC PTB of F665. Pharmacological modulation of this interaction may influence
 CC amyloid beta protein precursor metabolism. The invention provides protein
 CC complexes, identified by yeast two-hybrid screening, that comprise 2
 CC interacting proteins (or fragments), antibodies to the complexes,
 CC diagnosis of neurodegenerative disorders (including diagnosis of a
 CC predisposition to, or existence of, the disorder), drug screening for
 CC agents which modulate the protein interaction, and identification of
 CC additional proteins in the pathway common to the interacting proteins. A
 CC claimed method for treating a neurodegenerative disorder selected from
 CC Huntington's disease, Parkinson's disease, dementia and Alzheimer's
 CC disease involves administering a compound capable of modulating the
 CC protein complex. The compound may interfere with the protein interaction,
 CC bind one of the 2 proteins, may be an antibody immunoreactive with one of
 CC the proteins, or a nucleic acid encoding such an antibody, or is a
 CC compound that modulates expression of one of the proteins, is an
 CC antisense compound or ribozyme which hybridises to a nucleic acid
 CC encoding one of the proteins, or is a compound capable of strengthening
 CC the protein interaction (all claimed)
 XX
 XX Sequence 372 AA;
 PS
 XX Query Match 100.0%; Score 1951; DB 5; Length 372;
 CC Best Local Similarity 100.0%; Pred. No. 1.5e-206;
 CC Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 QY 1 MSTAALITLVRSNGQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRFPDGGSPAT 60
 Db 1 MSTAALITLVRSNGQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRFPDGGSPAT 60
 QY 61 WDNFGIWNDRIDEPILLPPSIKYGKIPKISLENVGCASQIGKRENERDFPAQLTDEV 120
 Db 61 WDNFGIWNDRIDEPILLPPSIKYGKIPKISLENVGCASQIGKRENERDFPAQLTDEV 120

QY 121 LYFAVYDGHGGPARADFCCHTHMEKICIMDLPEKKNLETLTLTAPLEIDKAFSSHARLSAD 180
 DB |||||||
 QY 121 LYFAVYDGHGGPARADFCCHTHMEKICIMDLPEKKNLETLTLTAPLEIDKAFSSHARLSAD 180
 DB |||||||
 QY 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
 DB |||||||
 QY 241 GGFVAVNSLGOPHYNGRLAMTRS:GDLDLKTSGVIAPEPKRIKLHADDSEFLVLTDDGI 300
 DB |||||||
 QY 301 NFMVNSQEICDFVNOCHDPNEAAHVAVTEQAIQYGTEDNSTAVVPPFGAWGKYKNSINF 360
 DB |||||||
 QY 361 FSRSPASSGRWA 372
 DB |||||||

RESULT 3

ABG70789
 ID ABG70789 standard; protein; 372 AA.

XX AC
 XX DT 12-DEC-2002 (first entry)
 XX DE Fe65 interacting human protein, PN7740, protein.

XX KW Yeast two-hybrid; PN7740; human; CIB; calcium-binding protein; MLK2;
 KW mixed lineage kinase 2; ligand; transporter; cellular uptake;
 KW neuronal death; neurodegenerative disorder; Huntington's disease;
 KW Parkinson's disease; dementia; Alzheimer's disease; APP; presenilin; PS1;
 KW PS2; Abeta; trophic; SAPP; metabolite; Fe65.

XX OS Homo sapiens.

XX PN US2002119927-A1.

XX PD 29-AUG-2002.

XX PF 09-OCT-2001; 2001US-00972757.

XX PR 17-OCT-2000; 2000US-0240790P.

XX PS (MYRI-) MYRIAD GENETICS INC.

XX PI Roch J, Bartel PL, Heichman K;

XX DR WPI; 2002-740204/80.

XX DR N-PSDB; ABS55204.

XX PT Modulating protein complex having proteins which is CIB interacting with
 PT mixed lineage kinase 2, in a cell, by administering compound that
 PT modulates the complex, or peptide that interferes interaction between
 PT proteins.

XX FS Example 6; Page 22; 37pp; English.

XX CC The invention discloses a method for modulating in a cell, a protein
 CC complex having a first protein, which is CIB (calcium-binding protein),
 CC interacting with a second protein, which is mixed lineage kinase (MLK)2,
 CC or the interaction of MLK2 with the ligand, which comprises administering
 CC to the cell a compound capable of modulating the protein complex or the
 CC interaction, or a peptide capable of interfering with the protein's
 CC interactions. The peptide is associated with a transporter capable of
 CC increasing cellular uptake of the peptide. The method is useful for
 CC modulating neuronal death in a patient having a neurodegenerative
 CC disorder such as Huntington's disease, Parkinson's disease, dementia and
 CC Alzheimer's disease. The technique used to discover additional proteins
 CC that interact with the major Alzheimer's disease proteins (including APP,

CC not defined, and presenilin) was the yeast two-hybrid system. CIB has
 CC been shown to interact with the presenilins, PS1 and PS2, but due to the
 CC casual role of mutations of these presenilins in Alzheimer's disease,
 CC other proteins, like MLK2, are likely to play a major role in the
 CC pathogenesis. APP metabolism is also a critical event in Alzheimer's
 CC disease pathogenesis as it leads to the release of either toxic (Abeta)
 CC or trophic (sAPP) metabolites. Fe65 (not defined) has been shown to
 CC interact with APP and peptides interacting with Fe65 may also be useful
 CC in treating neurodegenerative disorders. The compound may capable of
 CC strengthening the interaction between the first and the second protein.
 CC The sequence presented is the human PN7740 protein which was isolated due
 CC to its interaction with Fe65 found using the yeast two-hybrid system

XX SQ Sequence 372 AA;

Query Match 100.0%; Score 1951; DB 5; Length 372;

Best Local Similarity 100.0%; Pred. No. 1.5e-206;

Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSGNQVRRVLLSRLLQDDRRVPTCHSSTSEPRCGRFDPGSGSPAT 60
 DB 1 MSTAALITLVRSGNQVRRVLLSRLLQDDRRVPTCHSSTSEPRCGRFDPGSGSPAT 60
 QY 61 WDNFGIWDNRIDEPIILLPSIKYKPIPKISLNVGCSAQICKRKENEDRPFQALTDEV 120
 DB 61 WDNFGIWDNRIDEPIILLPSIKYKPIPKISLNVGCSAQICKRKENEDRPFQALTDEV 120
 QY 121 LYFAVYDGHGGPARADFCCHTHMEKICIMDLPEKKNLETLTLTAPLEIDKAFSSHARLSAD 180
 DB 121 LYFAVYDGHGGPARADFCCHTHMEKICIMDLPEKKNLETLTLTAPLEIDKAFSSHARLSAD 180
 QY 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
 DB 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
 QY 241 GGFVAVNSLGOPHYNGRLAMTRS:GDLDLKTSGVIAPEPKRIKLHADDSEFLVLTDDGI 300
 DB 241 GGFVAVNSLGOPHYNGRLAMTRS:GDLDLKTSGVIAPEPKRIKLHADDSEFLVLTDDGI 300
 QY 301 NFMVNSQEICDFVNOCHDPNEAAHVAVTEQAIQYGTEDNSTAVVPPFGAWGKYKNSINF 360
 DB 301 NFMVNSQEICDFVNOCHDPNEAAHVAVTEQAIQYGTEDNSTAVVPPFGAWGKYKNSINF 360
 QY 361 FSRSPASSGRWA 372
 DB 361 FSRSPASSGRWA 372

RESULT 4

AAE23953
 ID AAE23953 standard; protein; 372 AA.

XX AC AAE23953;

XX DT 23-SEP-2002 (first entry)

XX DE PN7740 protein.

XX OS Unidentified.
 KW Protein-protein interaction; neurodegenerative disorder; CIB; MLK2;
 KW Alzheimer's disease; calcium binding protein; mixed lineage kinase 2;
 KW Huntington's disease; dementia; Parkinson's disease; AD.

XX PN WO200233112-A2.

XX PD 25-APR-2002.

XX PF 16-OCT-2001; 2001WO-US032196.

XX PR 17-OCT-2000; 2000US-0240790P.

XX PS (MYRI-) MYRIAD GENETICS INC.

```
XX PI Roch J, Bartel PL, Heichman K;
XX DR WPI: 2002-454607/48.
XX DR N-PSDB; AAD38594.
XX
XX PT New protein complex comprising CIB and mixed lineage kinase 2, useful as
XX PT targets for diagnostic tools in identifying individuals at risk for
XX PT neurodegenerative disorders, e.g. Alzheimer's disease, Parkinson's
XX PT disease or dementia.
XX
XX PS Example 6; Page 52; 51pp; English.
XX
XX CC The invention relates to the discovery of protein-protein interactions
XX CC that are involved in the pathogenesis of neurodegenerative disorders
XX CC including Alzheimer's disease (AD). The invention is also directed to
XX CC protein complex comprising two proteins selected from a complex of
XX CC calcium binding protein (CIB) and mixed lineage kinase 2 (MLK2). AD
XX CC interacting proteins are useful as new targets for the identification of
XX CC useful pharmaceuticals, new targets for diagnostic tools in the
XX CC identification of individuals at risk, sequences for producing
XX CC transformed cell lines, cellular models and animal models and new bases
XX CC for therapeutic intervention in neurodegenerative disorders, including.
XX CC Modulators of the protein complex are useful for treating
XX CC neurodegenerative disorders including Huntington's disease, dementia,
XX CC Parkinson's disease and AD. The present sequence is PN7740 protein. This
XX CC sequence used in the exemplification of the invention
XX
XX SQ Sequence 372 AA;
XX
XX Query Match 100.0%; Score 1951; DB 5; Length 372;
XX Best Local Similarity 100.0%; Pred No. 1.5e-206;
XX Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRFPDPGSGSPAT 60
DB 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRFPDPGSGSPAT 60
QY 61 WDNFGIWDNRIDEPILLPPIKYGKPIKISLENVGCASQIGKRKNEDEDFDFAQLTDEV 120
DB 61 WDNFGIWDNRIDEPILLPPIKYGKPIKISLENVGCASQIGKRKNEDEDFDFAQLTDEV 120
QY 121 LYFAVYDGHGGAADAFCHTHMEKIMDLPEKKNLETLTLTFLAFLDKAFSSHARLSAD 180
DB 121 LYFAVYDGHGGAADAFCHTHMEKIMDLPEKKNLETLTLTFLAFLDKAFSSHARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVWASVGDSPAILCRKPKMKLTIDHTPERKDEKERIKKC 240
DB 181 ATLLTSGTTATVALLRDGIELVWASVGDSPAILCRKPKMKLTIDHTPERKDEKERIKKC 240
QY 241 GGFVAVNSLQGVHNGRLAMTRISGLDLKTSQVIAEPETKRIKLHADDPSFLVLTGDI 300
DB 241 GGFVAVNSLQGVHNGRLAMTRISGLDLKTSQVIAEPETKRIKLHADDPSFLVLTGDI 300
QY 301 NFVWNSQEIICDFVNOCHDNEAAHVAETQAIQYGTEDNSTAVVPPGAWKYNSEINFS 360
DB 301 NFVWNSQEIICDFVNOCHDNEAAHVAETQAIQYGTEDNSTAVVPPGAWKYNSEINFS 360
QY 361 FSRSFASSGRWA 372
DB 361 FSRSFASSGRWA 372
XX
XX RESULT 5
XX ABG70801
XX ID ABG70801 standard; protein; 372 AA.
XX AC ABG70801;
XX XX
XX DT 16-DEC-2002 (first entry)
XX DE Fe65 interacting human protein, PN7740, protein.
XX XX
```

```
KW Yeast two-hybrid; PN7740; human; Mint2; PDE-9A; KIAA0427; ligand;
KW transporter; cellular uptake; neuronal death; neurodegenerative disorder;
KW Huntington's disease; Parkinson's disease; dementia; Alzheimer's disease;
KW APP; presenilin; Abeta; trophic; SAPP; metabolite; Fe65.
XX OS Homo sapiens.
XX XX
XX FN US2002114799-A1.
XX XX
XX PD 22-AUG-2002.
XX
XX PF 10-OCT-2001; 2001US-00973077.
XX
XX PR 17-OCT-2000; 2000US-0240790P.
XX
XX PA (MYRI-) MYRIAD GENETICS INC.
XX
XX PI Roch J, Bartel PL, Heichman K;
XX
XX DR WPI: 2002-740090/80.
XX DR N-PSDB; ABS55222.
XX
XX PT Modulating protein complex having Mint2 interacting with PDE-9A, by
XX PT administering compound capable of modulating protein complex, or peptide
XX PT capable of interfering with protein-protein interaction.
XX
XX PS Example 6; Page 22; 37pp; English.
XX
XX CC The invention discloses a method for modulating in a cell, a protein
XX CC complex having a first protein, which is Mint2, interacting with a second
XX CC protein, which is PDE-9A, or the interaction of PDE-9A with the ligand,
XX CC which comprises administering to the cell a compound capable of
XX CC modulating the protein complex or the interaction, or a peptide capable
XX CC of interfering with the protein's interactions. The peptide is associated
XX CC with a transporter capable of increasing cellular uptake of the peptide.
XX CC The method is useful for modulating neuronal death in a patient having a
XX CC neurodegenerative disorder such as Huntington's disease, Parkinson's
XX CC disease, dementia and Alzheimer's disease. The technique used to discover
XX CC additional proteins that interact with the major Alzheimer's disease
XX CC proteins (including APP, not defined, and presenilins) was the yeast
XX CC hybrid system. Mint2 has been shown to interact with APP, and due its
XX CC interaction with presenilins and KIAA0427 it is likely to play a major
XX CC role in the pathogenesis of Alzheimer's disease. APP metabolism is also a
XX CC critical event in Alzheimer's disease pathogenesis as it leads to the
XX CC release of either toxic (Abeta) or trophic (sAPP) metabolites. Fe65 (not
XX CC defined) has been shown to interact with APP and peptides interacting
XX CC with Fe65 may also be useful in treating neurodegenerative disorders. The
XX CC compound may be capable of strengthening the interaction between the first
XX CC and the second protein. The sequence presented is the human PN7740
XX CC protein which was isolated due to its interaction with Fe65 found using
XX CC the yeast two-hybrid system
XX
XX SQ Sequence 372 AA;
XX
XX Query Match 100.0%; Score 1951; DB 5; Length 372;
XX Best Local Similarity 100.0%; Pred No. 1.5e-206;
XX Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRFPDPGSGSPAT 60
DB 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRFPDPGSGSPAT 60
QY 61 WDNFGIWDNRIDEPILLPPIKYGKPIKISLENVGCASQIGKRKNEDEDFDFAQLTDEV 120
DB 61 WDNFGIWDNRIDEPILLPPIKYGKPIKISLENVGCASQIGKRKNEDEDFDFAQLTDEV 120
QY 121 LYFAVYDGHGGAADAFCHTHMEKIMDLPEKKNLETLTLTFLAFLDKAFSSHARLSAD 180
DB 121 LYFAVYDGHGGAADAFCHTHMEKIMDLPEKKNLETLTLTFLAFLDKAFSSHARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVWASVGDSPAILCRKPKMKLTIDHTPERKDEKERIKKC 240
DB 181 ATLLTSGTTATVALLRDGIELVWASVGDSPAILCRKPKMKLTIDHTPERKDEKERIKKC 240
XX
```

QY 241 GGFVAVNSLGQPHVNGRLATRSIGDLTKTSQVIAPETPKRIKLHADDSEFLVLTDDGI 300
DB 241 GGFVAVNSLGQPHVNGRLATRSIGDLTKTSQVIAPETPKRIKLHADDSEFLVLTDDGI 300
QY 301 NFMVNSQICDFVNOCHDPNEAAHVAHQIYGTEDNSTAVVPPFGAWGKYKNSSEINFS 360
DB 301 NFMVNSQICDFVNOCHDPNEAAHVAHQIYGTEDNSTAVVPPFGAWGKYKNSSEINFS 360
QY 361 FSRSPASSGRWA 372
DB 361 FSRSPASSGRWA 372

RESULT 6
ID ABG70826 standard; protein; 372 AA.
XX
AC ABG70826;
XX
DI 17-DEC-2002 (first entry)
XX
DE Fe65 interacting human protein, PN7740, protein.
XX
KW Yeast two-hybrid; PN7740; human; CIB; calcium-binding protein; MLK2;
KW mixed lineage kinase 2; ligand; transporter; cellular uptake;
KW neuronal death; neurodegenerative disorder; Huntington's disease;
KW Parkinson's disease; dementia; Alzheimer's disease; APP; presenilin; PS1;
KW PS2; Abeta; trophic; sAPP; metabolite; Fe65.
XX
OS Homo sapiens.
XX
PN US2002119155-A1.
XX
PD 29-AUG-2002.
XX
PF 09-OCT-2001; 2001US-00972038.
XX
PR 17-OCT-2000; 2000US-0240790P.
XX
PA (MTRI-) MYRIAD GENETICS INC.
XX
PI Roch J, Bartel PL, Heichman K;
XX
DR WPI; 2002-750045/81.
DR N-PSDB; ABS55238.
XX
PT Novel protein complex useful for screening for drug that modulates
PT interaction of the proteins, has two proteins chosen from a complex of
PT CIB or its fragment, and mixed lineage kinase 2 or its fragment.
XX
PS Example 6; Page 22; 36pp; English.

CC The invention discloses an isolated protein complex comprising two
CC proteins, chosen from a complex of CIB (calcium-binding protein), or its
CC fragment, and mixed lineage kinase 2 (MLK2), or its fragment. The complex
CC is useful for diagnosing a neurodegenerative disorder in an animal, by
CC assaying whether the protein complex is present in a tissue extract, the
CC ability of proteins to form the complex and a mutation in a gene encoding
CC a protein of the complex and for determining whether a mutation in a gene
CC encoding one of the proteins of the complex is useful for diagnosing a
CC neurodegenerative disorder, where the inability to form the complex is
CC indicative of the mutation. The complex is also useful for diagnosing
CC (predisposition or existence of) neurodegenerative disorders such as
CC Huntington's disease, Parkinson's disease, dementia and Alzheimer's
CC disease, in humans, for screening for drug candidates that are capable of
CC modulating the interaction of the first and second proteins, for the
CC generation of antibodies, for the identification of agents that are
CC capable of modulating the interactions, which are useful for treating the
CC above mentioned neurodegenerative disorders and for screening individuals
CC who are at risk of developing neurodegenerative disorders. The technique
CC used to discover additional proteins that interact with the major
CC Alzheimer's disease proteins (including APP, not defined, and

CC presenilins) was the yeast two-hybrid system. CIB has been shown to
CC interact with the presenilins, PS1 and PS2, but due to the casual role of
CC mutations of these presenilins in Alzheimer's disease, other proteins,
CC like MLK2, are likely to play a major role in the pathogenesis. APP
CC metabolism is also a critical event in Alzheimer's disease pathogenesis
CC as it leads to the release of either toxic (Abeta) or trophic (sAPP)
CC metabolites. Fe65 (not defined) has been shown to interact with APP and
CC peptides interacting with Fe65 may also be useful in treating
CC neurodegenerative disorders. The sequence presented is the human PN7740
CC protein which was isolated due to its interaction with Fe65 found using
CC the yeast two-hybrid system
XX
SQ Sequence 372 AA;

Query Match 100.0%; Score 1951; DB 5; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.5e-206;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSTAALITLVRSQGNQVRRVLLSRLQLDDRRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60
DB 1 MSTAALITLVRSQGNQVRRVLLSRLQLDDRRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60
QY 61 WDNFGIWNDRIDEPIILLPPSIKYKPIPIKISLNVGCSAQIGKRKENEDRFDPAQLTDEV 120
DB 61 WDNFGIWNDRIDEPIILLPPSIKYKPIPIKISLNVGCSAQIGKRKENEDRFDPAQLTDEV 120
QY 121 LYPVAVDGHGGAADAFCHTHMEKICIMDLKPKEKLETLTLTAFLEIDKAFSSHARLSAD 180
DB 121 LYPVAVDGHGGAADAFCHTHMEKICIMDLKPKEKLETLTLTAFLEIDKAFSSHARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVAVSDSRAILCRKGKPKMLTIDHTPERKDEKERIKK 240
DB 181 ATLLTSGTTATVALLRDGIELVAVSDSRAILCRKGKPKMLTIDHTPERKDEKERIKK 240
QY 241 GGFVAVNSLGQPHVNGRLATRSIGDLTKTSQVIAPETPKRIKLHADDSEFLVLTDDGI 300
DB 241 GGFVAVNSLGQPHVNGRLATRSIGDLTKTSQVIAPETPKRIKLHADDSEFLVLTDDGI 300
QY 301 NFMVNSQICDFVNOCHDPNEAAHVAHQIYGTEDNSTAVVPPFGAWGKYKNSSEINFS 360
DB 301 NFMVNSQICDFVNOCHDPNEAAHVAHQIYGTEDNSTAVVPPFGAWGKYKNSSEINFS 360
QY 361 FSRSPASSGRWA 372
DB 361 FSRSPASSGRWA 372

RESULT 7
ABG07402
ID ABB07402 standard; protein; 372 AA.
XX
AC ABB07402;
XX
DT 09-APR-2002 (first entry)
XX
DE Human protein phosphatase IIC AB12 polypeptide.
XX
KW Protein phosphatase IIC AB12; antiasthmatic; antiapoptotic; anti-HIV;
KW neuroprotective; vasotropic; virucide; osteopathic; cytostatic; human;
KW antiinflammatory; anabolic; cancer.
XX
OS Homo sapiens.
XX
PN WO2001196571-A2.
XX
PD 20-DEC-2001.
XX
PF 13-JUN-2001; 2001WO-EF006666.
XX
PR 16-JUN-2000; 2000US-0212043P.
PR 07-AUG-2000; 2000US-0223322P.
PR 13-DEC-2000; 2000US-0254877P.
XX

PA (FARB) BAYER AG.
 PI Xiao Y;
 XX
 XX
 DR WPI; 2002-139713/18.
 XX
 XX Protein phosphatase IIC ABI2 polypeptide and polynucleotides useful for
 PT identifying modulating agents useful in treating diseases e.g. cancer,
 PT inflammatory disorder, osteoporosis, asthma, AIDS and viral infections.
 XX
 XX Claim 26; Fig 19; 135pp; English.
 PS
 XX The invention relates to human protein phosphatase IIC ABI2 polypeptides
 CC and polynucleotides. The polypeptides can be expressed by standard
 CC recombinant methodology. The polypeptides, polynucleotides and modulators
 CC are useful for modulating activity of protein phosphatase IIC ABI2 in a
 CC disease or treating a disease which include asthma, chronic obstructive
 CC pulmonary disease (COPD), peripheral or central nervous system disease
 CC including neurodegenerative disease, a disorder associated with an
 CC increase in apoptosis, including AIDS and other infectious or genetic
 CC immunodeficiency, myelodysplasia, ischemic injury, toxin-induced disease,
 CC wasting disease, viral infection and osteoporosis; or disorder associated
 CC with decrease in apoptosis, including cancer and inflammatory disorder.
 CC Fusion proteins comprising protein phosphatase IIC ABI2 are useful for
 CC generating antibodies and for use in various assay systems, and the
 CC protein phosphatase IIC ABI2 polypeptide can also be used as a bait
 CC protein in a two-hybrid assay or three-hybrid assay. The present sequence
 CC represents a human protein phosphatase IIC ABI2 polypeptide
 XX
 XX SQ Sequence 372 AA;
 Query Match 100.0%; Score 1951; DB 5; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.5e-206;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSTAALITLVRSNGNVRRLVSSRLQLDQRRVPTCHSSTSEPCSRFPDGGSPAT 60
 DB 1 MSTAALITLVRSNGNVRRLVSSRLQLDQRRVPTCHSSTSEPCSRFPDGGSPAT 60
 QY 61 WDNFGIWDNRIDEPILLPSPKIYKGPPIKISLENVGCASQIGKRKENEFRDFAQLTDEV 120
 DB 61 WDNFGIWDNRIDEPILLPSPKIYKGPPIKISLENVGCASQIGKRKENEFRDFAQLTDEV 120
 QY 121 LYFAVDGHHGPPAAADFCHTHMEKCIIMDLKPKEKNLETLTLTFLAFLIDKAFSSHARLSAD 180
 DB 121 LYFAVDGHHGPPAAADFCHTHMEKCIIMDLKPKEKNLETLTLTFLAFLIDKAFSSHARLSAD 180
 QY 181 ATLLTSGTTATVALLRDGIELVWASVGDSPAILCRKKGPKMLTIDHTPERKDEKERIKKC 240
 DB 181 ATLLTSGTTATVALLRDGIELVWASVGDSPAILCRKKGPKMLTIDHTPERKDEKERIKKC 240
 QY 241 GGFVAMNSLGQPHVNGRLAMTRISGDLDTKTSVIAEPETKRIKLHADDSEFLVLTDDGI 300
 DB 241 GGFVAMNSLGQPHVNGRLAMTRISGDLDTKTSVIAEPETKRIKLHADDSEFLVLTDDGI 300
 QY 301 NFVNSQEIICDFVNOCHDPNEAAHVAHQIAQYGTEDNSTAVVVPFGANGKYKNSINFS 360
 DB 301 NFVNSQEIICDFVNOCHDPNEAAHVAHQIAQYGTEDNSTAVVVPFGANGKYKNSINFS 360
 QY 361 FRSFASGSGWA 372
 DB 361 FRSFASGSGWA 372
 RESULT 8
 AAE23976
 ID AAE23976 standard; protein; 372 AA.
 XX
 XX AAE23976;
 AC
 XX
 DT 23-SEP-2002 (first entry)
 XX
 XX Human PN7740 protein.

XX Human; protein-protein interaction; neurodegenerative disorder;
 KW Alzheimer's disease; AD; pharmaceutical; Huntington's disease;
 KW Parkinson's disease; anticonvulsant; dementia; neuroprotective;
 KW nootropic; PN7740.
 XX
 OS Homo sapiens.
 PN WO200233113-A2.
 XX
 XX 25-APR-2002.
 XX
 XX 16-OCT-2001; 2001WO-US032197.
 XX
 PR 17-OCT-2000; 2000US-0240790P.
 XX
 XX (MYRI-) MYRIAD GENETICS INC.
 PA
 XX Roch J, Bartel PL, Heichman K;
 PI WPI; 2002-454608/48.
 DR N-PSDB; AAD38691.
 XX
 XX New protein complex comprising Mint2 and PDE-9A proteins, useful as
 PT targets for diagnostic tools in identifying individuals at risk for
 PT neurodegenerative disorders, e.g. Alzheimer's disease, Parkinson's
 PT disease, or dementia.
 XX
 XX Example 6; Page 52; 91pp; English.
 PS
 XX The invention relates to the discovery of protein-protein interactions
 CC that are involved in the pathogenesis of neurodegenerative disorders,
 CC including Alzheimer's disease (AD). The AD interacting proteins are,
 CC useful as new targets for the identification of useful pharmaceuticals,
 CC new targets for diagnostic tools in the identification of individuals at
 CC risk, sequences for producing transformed cell lines, cellular models and
 CC animal models, and new bases for therapeutic intervention in
 CC neurodegenerative disorders, particularly AD. The DNA encoding the
 CC protein of the invention can be used to create animals that overexpress
 CC the protein, or animals which do not express the native gene but express
 CC the protein. Modulators of the protein complex are useful for treating a
 CC neurodegenerative disorder including Huntington's disease, Parkinson's
 CC disease, dementia or Alzheimer's disease. The present sequence is human
 CC PN7740 protein used in the exemplification of the invention
 XX
 XX SQ Sequence 372 AA;
 Query Match 100.0%; Score 1951; DB 5; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.5e-206;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSTAALITLVRSNGNVRRLVSSRLQLDQRRVPTCHSSTSEPCSRFPDGGSPAT 60
 DB 1 MSTAALITLVRSNGNVRRLVSSRLQLDQRRVPTCHSSTSEPCSRFPDGGSPAT 60
 QY 61 WDNFGIWDNRIDEPILLPSPKIYKGPPIKISLENVGCASQIGKRKENEFRDFAQLTDEV 120
 DB 61 WDNFGIWDNRIDEPILLPSPKIYKGPPIKISLENVGCASQIGKRKENEFRDFAQLTDEV 120
 QY 121 LYFAVDGHHGPPAAADFCHTHMEKCIIMDLKPKEKNLETLTLTFLAFLIDKAFSSHARLSAD 180
 DB 121 LYFAVDGHHGPPAAADFCHTHMEKCIIMDLKPKEKNLETLTLTFLAFLIDKAFSSHARLSAD 180
 QY 181 ATLLTSGTTATVALLRDGIELVWASVGDSPAILCRKKGPKMLTIDHTPERKDEKERIKKC 240
 DB 181 ATLLTSGTTATVALLRDGIELVWASVGDSPAILCRKKGPKMLTIDHTPERKDEKERIKKC 240
 QY 241 GGFVAMNSLGQPHVNGRLAMTRISGDLDTKTSVIAEPETKRIKLHADDSEFLVLTDDGI 300
 DB 241 GGFVAMNSLGQPHVNGRLAMTRISGDLDTKTSVIAEPETKRIKLHADDSEFLVLTDDGI 300
 QY 301 NFVNSQEIICDFVNOCHDPNEAAHVAHQIAQYGTEDNSTAVVVPFGANGKYKNSINFS 360
 DB 301 NFVNSQEIICDFVNOCHDPNEAAHVAHQIAQYGTEDNSTAVVVPFGANGKYKNSINFS 360

Db 301 NFMVNSQEICDFVNOCHDPNEAAHVAITEQAIQYGTEDNSTAVVVPFGAWGKYKNSINFS 360
 Qy 361 FSRSPASSGRWA 372
 Db 361 FSRSPASSGRWA 372

RESULT 9
 AAE24078
 ID AAE24078 standard; protein; 372 AA.
 XX
 AC AAE24078;
 XX
 DT 04-OCT-2002 (first entry)
 XX
 DE Human PN7740 protein.
 XX
 KW Protein complex; postsynaptic density protein; PSD95; Fe65; dementia;
 KW neurodegenerative disorder; Huntington's disease; Parkinson's disease;
 KW PN7740; Alzheimer's disease; drug designing; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200232286-A2.
 XX
 PD 25-APR-2002.
 XX
 PF 16-OCT-2001; 2001WO-US032186.
 XX
 PR 17-OCT-2000; 2000US-0240790P.
 PR 13-JUL-2001; 2001US-0304775P.
 XX
 PA (MYRI-) MYRIAD GENETICS INC.
 XX
 PI Roch J, Bartel PL, Heichman K;
 XX
 DR WPI; 2002-479640/51.
 DR N-PSDB; AAD39176.
 XX
 PT Novel isolated protein complex having a protein which is postsynaptic
 PT density protein or Fe65 interacting with another protein which is PN7740
 PT useful for drug designing for treating neurodegenerative disorder.
 XX
 PS Claim 24; Page 52; 102pp; English.
 XX

The invention relates to an isolated protein complex having a first
 protein which is postsynaptic density protein (PSD95) or Fe65 interacting
 with a second protein which is PN7740. Protein complex of the invention
 is useful for diagnosing a neurodegenerative disorder in human, for
 determining a predisposition to the neuro- degenerative disorder or for
 the existence of the disorder. They are used for treating degenerative
 disorders such as Huntington's disease, Parkinson's disease, dementia and
 Alzheimer's disease. They are also used for drug designing and for
 screening compounds that modulate the interaction of proteins of the
 invention. The present sequence is human PN7740 protein

XX Sequence 372 AA;
 Qy
 Query Match 100.0%; Score 1951; DB 5; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.5e-206;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTAALTLVRSGNQVRRVLLSRLLQDDRRVPTCHSSTSEPRCSRPDPGSGSPAT 60
 Db 1 MSTAALTLVRSGNQVRRVLLSRLLQDDRRVPTCHSSTSEPRCSRPDPGSGSPAT 60
 Qy 61 WDNFGIWNDRIDEPIILLPPSIKYGKPIKISLENVGCSAQIGKKEKNEFRDFAQLTDEV 120
 Db 61 WDNFGIWNDRIDEPIILLPPSIKYGKPIKISLENVGCSAQIGKKEKNEFRDFAQLTDEV 120
 Qy 121 LYFAVYDGHGGPAAADFCFTHMEKICIMDLLPKKXNLETLLTFLAPLEIDKAFSSHARLSAD 180
 Db 121 LYFAVYDGHGGPAAADFCFTHMEKICIMDLLPKKXNLETLLTFLAPLEIDKAFSSHARLSAD 180

Qy 181 ATLLTSGTTATVALLRDGIELVWASVGSRAILCRKGPKMLTIDHTPERKDEKERIKK 240
 Db 181 ATLLTSGTTATVALLRDGIELVWASVGSRAILCRKGPKMLTIDHTPERKDEKERIKK 240
 Qy 241 GGFVAVNSLQOPHVNGRLAMTRESIGDLDKTSGVIAEPETKRIKLHADDSEFLVLTDDGI 300
 Db 241 GGFVAVNSLQOPHVNGRLAMTRESIGDLDKTSGVIAEPETKRIKLHADDSEFLVLTDDGI 300
 Qy 301 NFMVNSQEICDFVNOCHDPNEAAHVAITEQAIQYGTEDNSTAVVVPFGAWGKYKNSINFS 360
 Db 301 NFMVNSQEICDFVNOCHDPNEAAHVAITEQAIQYGTEDNSTAVVVPFGAWGKYKNSINFS 360
 Qy 361 FSRSPASSGRWA 372
 Db 361 FSRSPASSGRWA 372

RESULT 10
 AAE14451
 ID AAE14451 standard; protein; 372 AA.
 XX
 AC AAE14451;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human protein phosphatase-1.
 XX
 KW Human; protein phosphatase; PP-1; immune system disorder; AIDS; allergy;
 KW neurological disorder; developmental disorder; Alzheimer's disease;
 KW cell proliferative disorder; Huntington's disease; arteriosclerosis;
 KW renal tubular acidosis; gonadal dysgenesis; cancer; adenocarcinoma;
 KW leukaemia; transgenic animal; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 104..339
 FT /note= "Protein phosphatase 2C (Pp2C)"
 FT Domain 122..130
 FT /label= Protein_phosphatase_2C_motif
 XX
 PN WO200196546-A2.
 XX
 PD 20-DEC-2001.
 XX
 PF 14-JUN-2001; 2001WO-US019442.
 XX
 PR 16-JUN-2000; 2000US-0212447P.
 PR 22-JUN-2000; 2000US-0213746P.
 PR 29-JUN-2000; 2000US-0215210P.
 PR 06-JUL-2000; 2000US-0215299P.
 PR 12-JUL-2000; 2000US-0218080P.
 PR 21-JUL-2000; 2000US-0220117P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Au-Young J, Baughn MR, Ding L, Elliott VS, Gandhi AR, Griffin JA;
 PI Hafalia A, Kearney L, Lee EA, Lu Y, Nguyen DB, Patterson C;
 PI Ramkumar J, Reddy R, Sanjanwala MS, Stewart EA, Tang YT, Thornton M;
 PI Tribouley CM, Wallia NK, Yang J, Yao MG, Yue H;
 XX
 DR WPI; 2002-090206/12.
 DR N-PSDB; AAD24019.
 XX
 PT Novel polypeptide, useful for diagnosing, treating or preventing
 PT disorders of growth and development, immune system, neurological and cell
 PT proliferation diseases, comprises cancer protein phosphatase
 PT polypeptides.
 XX
 PS Claim 1; Page 102-103; 116pp; English.
 XX
 CC The present sequence is human protein phosphatase (PP)-1. PP

CC polynucleotide and polypeptide are useful in the diagnosis, treatment and
 CC prevention of immune system disorders, neurological disorders,
 CC developmental disorders and cell proliferative disorders. Examples of
 CC immune system disorders include acquired immune deficiency syndrome
 CC (AIDS), severe combined immunodeficiency disease (SCID), adult
 CC respiratory distress syndrome, allergies, amyloidosis, anaemia, asthma,
 CC atherosclerosis, Crohn's disease, atopic dermatitis, diabetes mellitus,
 CC emphysema, Goodpasture's syndrome, gout, Graves' disease, multiple
 CC sclerosis, myasthenia gravis, myocardial or pericardial inflammation,
 CC osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,
 CC rheumatoid arthritis, Sjogren's syndrome, scleroderma, systemic
 CC sclerosis, trauma, neurological disorders include Alzheimer's disease,
 CC Huntington's disease, dementia, epilepsy, Parkinson's disease, mental
 CC retardation and other developmental disorders of central nervous system
 CC such as Down's syndrome, cerebral palsy, periodic paralysis, mental
 CC disorders including mood, anxiety, and schizophrenic disorders, seasonal
 CC affective disorder such as akathisia, amnesia, catatonia, dyskinesia;
 CC developmental disorders include e.g. renal tubular acidosis, Duchenne and
 CC Becker muscular dystrophy, gonadal dysgenesis, hypothyroidism; cell
 CC proliferative disorders include e.g. actinic keratosis, arteriosclerosis,
 CC atherosclerosis, bursitis, cirrhosis, hepatitis, psoriasis and cancer
 CC including adenocarcinoma, leukaemia. The polypeptide and polynucleotide
 CC are further useful for analysing proteome of a tissue or a cell type, for
 CC screening an agonist/antagonist, a compound that specifically binds to it
 CC or its modulator. The polynucleotide is useful for creating knockin
 CC humanised animals (pigs) or transgenic animals (mice or rats) to model
 CC human disease, for generating a transcript image of a tissue or cell
 CC type, which represents the global pattern of gene expression by a
 CC particular tissue or cell type
 XX
 XX Sequence 372 AA;

Query Match 100.0%; Score 1951; DB 5; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.5e-206;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNQVRRVLLSRLLQDDRRVPTCHSSTSEPCRSFDPDGGSPAT 60
 DB 1 MSTAALITLVRSQGNQVRRVLLSRLLQDDRRVPTCHSSTSEPCRSFDPDGGSPAT 60

QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLVNVCASQIGKRNEDRFDFAQLTDEV 120
 DB 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLVNVCASQIGKRNEDRFDFAQLTDEV 120

QY 121 LYFAVDGHHGGAADFCFTHMEKIMDLPKEKNLETLTLTAFLEIDKATSSHARLSAD 180
 DB 121 LYFAVDGHHGGAADFCFTHMEKIMDLPKEKNLETLTLTAFLEIDKATSSHARLSAD 180

QY 181 ATLLTSGTTATVALLRDGIELVAVSGDSRAILCRKGPMLTIDHTPERKDEKERIKKC 240
 DB 181 ATLLTSGTTATVALLRDGIELVAVSGDSRAILCRKGPMLTIDHTPERKDEKERIKKC 240

QY 241 GGFVANSIGQPHVNGRLAWTSIGDLDTKTSVTAEPETKRIKLHADDLFLVLTDDGI 300
 DB 241 GGFVANSIGQPHVNGRLAWTSIGDLDTKTSVTAEPETKRIKLHADDLFLVLTDDGI 300

QY 301 NFVNSQIEICDFVNOCHDNEAAHVAHQAIQYGTEDNSTAVVFPFGAWGKYKSEINFS 360
 DB 301 NFVNSQIEICDFVNOCHDNEAAHVAHQAIQYGTEDNSTAVVFPFGAWGKYKSEINFS 360

QY 361 FSRSPASSGRWA 372
 DB 361 FSRSPASSGRWA 372

RESULT 11
 ID ABU10309
 XX ABU10309 standard; protein; 372 AA.

AC ABU10309;
 XX
 XX 07-AUG-2003 (first entry)
 XX

Human protein phosphatase SGP037.
 Human; protein phosphatase; SGP037; cancer; blood; haematopoietic;
 KW breast; colon; lung; prostate; cervical; brain; ovarian; bladder; kidney;
 KW immune-related disease; cardiovascular disease; migraine;
 KW neuronal-associated disease; nervous system disease; pain; rhinitis;
 KW sexual dysfunction; mood disorder; attention disorder; hypotension;
 KW cognition disorder; hypertension; psychotic disorder; dyskinesia;
 KW neurological disorder; metabolic disorder; inflammatory disorder;
 KW rheumatoid arthritis; chronic inflammatory bowel disease; asthma;
 KW chronic inflammatory pelvic disease; multiple sclerosis; psoriasis;
 KW osteoarthritis; psoriasis; atherosclerosis; autoimmunity; nocropic;
 KW organ transplant rejection; cytostatic; neuroprotective; analgesic;
 KW hypotensive; anticonvulsant; antiarthritic; antirheumatic;
 KW antiinflammatory; antilasthmatic; osteopathic; antipsoriatic;
 KW antiarteriosclerotic; immunosuppressive; enzyme.

OS Homo sapiens.
 XX
 XX US2003027308-A1.
 XX
 XX 06-FEB-2003.
 XX
 XX 13-NOV-2001; 2001US-00986992.
 XX
 XX 30-MAY-2000; 2000US-0208291P.
 XX 13-NOV-2000; 2000US-0246974P.
 XX
 XX (SUGE-) SUGEN INC.

XX Plowman GD, Whyte D, Manning G;

XX WPI; 2003-456146/44.
 XX N-PSDB; ABX95873.

XX New isolated, enriched or purified nucleic acid molecule encoding a
 XX phosphatase polypeptide, useful for treating diseases, e.g. cancers, or
 XX immune-related, cardiovascular, brain and neuronal, metabolic or
 XX inflammatory disorders.

XX Claim 1; Fig 2; 45pp; English.

XX The present invention relates to the isolation of a novel human protein
 XX phosphatase designated SGP037, and the polynucleotide sequence encoding
 XX it. The gene encoding human SGP037 maps to chromosome 4q21. The SGP037
 XX polypeptide and the polynucleotide sequence encoding it are useful for
 XX treating diseases or disorders such as cancers (e.g. cancer of the blood
 XX or haematopoietic origin, breast, colon, lung, prostate, cervical, brain,
 XX ovarian, bladder or kidney), immune-related diseases and disorders,
 XX cardiovascular diseases, brain and neuronal-associated diseases (e.g.
 XX central or peripheral nervous system diseases, migraines, pain, sexual
 XX dysfunction, mood disorders, attention disorders, cognition disorders,
 XX dyskinesias), metabolic disorders, and inflammatory disorders (e.g.
 XX rheumatoid arthritis, chronic inflammatory bowel disease, chronic
 XX inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
 XX psoriasis, atherosclerosis, rhinitis, autoimmunity or organ transplant
 XX rejection). The present sequence represents human SGP037

XX Sequence 372 AA;

Query Match 100.0%; Score 1951; DB 6; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.5e-206;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNQVRRVLLSRLLQDDRRVPTCHSSTSEPCRSFDPDGGSPAT 60
 DB 1 MSTAALITLVRSQGNQVRRVLLSRLLQDDRRVPTCHSSTSEPCRSFDPDGGSPAT 60

QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLVNVCASQIGKRNEDRFDFAQLTDEV 120
 DB 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLVNVCASQIGKRNEDRFDFAQLTDEV 120

QY 121 LYFAVYDGHGGPAAADFCFTHMEKICIMDLPLPKKXKLETLTLAFLEIDKAFSSHARLSAD 180
DB 121 LYFAVYDGHGGPAAADFCFTHMEKICIMDLPLPKKXKLETLTLAFLEIDKAFSSHARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVWASVGDSSRAILCRKKGPKMLTIDHTPERKDEKERIKKC 240
DB 181 ATLLTSGTTATVALLRDGIELVWASVGDSSRAILCRKKGPKMLTIDHTPERKDEKERIKKC 240
QY 241 GGFVAMNSLGQPHVNGRLAMTRSGDLDLKTSVGIABPETYKRIKLHHADDSFLVLTDDGI 300
DB 241 GGFVAMNSLGQPHVNGRLAMTRSGDLDLKTSVGIABPETYKRIKLHHADDSFLVLTDDGI 300
QY 301 NFMVNSQEICDFVNOCHDPNEAAHVAITEQAIQYGTEDNSTAVVVPFGAWGKYKNSSEINFS 360
DB 301 NFMVNSQEICDFVNOCHDPNEAAHVAITEQAIQYGTEDNSTAVVVPFGAWGKYKNSSEINFS 360
QY 361 FRSFPASSGRWA 372
DB 361 FRSFPASSGRWA 372

RESULT 12
AAO23055
ID AAO23055 standard; protein; 372 AA.
AC AAO23055;
XX
DT 17-SEP-2003 (first entry)
XX
DE Human serine/threonine PP2C phosphatase SGP037 protein.
XX
KW Cytostatic; immunosuppressive; cardiovascular; hypotensive; hypertensive;
KW antimigraine; analgesic; nootropic; tranquiliser; antirheumatic; brain;
KW antiarthritic; antiinflammatory; gynaecological; neuroprotective; ocular;
KW antiasthmatic; osteopathic; antipsoriatic; antiarteriosclerotic; obesity;
KW antiallergic; serine threonine phosphatase; STP; PP2C; cancer; immune;
KW cardiovascular disease; neuronal; sexual dysfunction; migraine; glaucoma;
KW psychotic; neurological; schizophrenia; metabolic; inflammatory; SGP037;
KW multiple sclerosis; viral infection; HIV; transgenic; gene therapy;
KW enzyme; human; chromosome 4q21.
XX
OS Homo sapiens.
XX
FH Key
FT Region
FT 104..339
FT /note= "Catalytic region"
XX
PN WO2003042390-A1.
XX
PD 22-MAY-2003.
XX
PF 13-NOV-2001; 2001WO-US043063.
XX
PR 13-NOV-2001; 2001WO-US043063.
XX
PA (PLOW/) PLOWMAN G D.
XX
PI Plowman GD, Manning G, Whyte D;
XX
DR WPI; 2003-449576/42.
DR N-PSDB; AAL55773.
XX
PT New phosphatase nucleic acid molecule and polypeptide, useful for
PT diagnosing or treating phosphates-related disorders such as cancers,
PT immune-related disorders, cardiovascular disease, and inflammatory
PT disorders.
XX
PS Claim 26; Fig 2; 152pp; English.
XX
CC The invention relates to a novel isolated nucleic acid molecule encoding
CC a serine/threonine phosphatase (STP) polypeptide which is a member of the
CC PP2C family. PP2C phosphatases are involved in a number of cellular
CC processes including modulation of integrin signal transduction and

CC regulation of the TAK1 signalling pathway, cellular channels, cyclin
CC dependent kinases and the Ras pathway. The methods and compositions of
CC the present invention may be useful during the diagnosis or treatment of
CC a variety of disorders including cancers, immune-related and
CC cardiovascular disease, brain or neuronal-associated diseases such as
CC sexual dysfunction and migraine, psychotic and neurological disorders
CC e.g. schizophrenia and metabolic disorders such as obesity. Furthermore,
CC ocular disease, such as glaucoma and inflammatory disorders e.g. multiple
CC sclerosis may be addressed, as well as viral infections caused by HIV and
CC other pathological agents. Finally, the molecules of the invention may be
CC utilised in the production of transgenic animals and during gene therapy.
CC The current sequence is that of the human serine/threonine PP2C
CC phosphatase SGP037 protein of the invention
XX
SQ Sequence 372 AA;

Query Match 100.0%; Score 1951; DB 6; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.5e-206;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSTAALITLVRSQGVRRVLLSSRLQLQDDRRVPTCHSSTSEPRCSRFPDGGSPAT 60
DB 1 MSTAALITLVRSQGVRRVLLSSRLQLQDDRRVPTCHSSTSEPRCSRFPDGGSPAT 60
QY 61 WDNFGIWNDRIDEPIILLPESIKYGRPIPKISLENVGCASQICKRKENEDRFPDLTDEV 120
DB 61 WDNFGIWNDRIDEPIILLPESIKYGRPIPKISLENVGCASQICKRKENEDRFPDLTDEV 120
QY 121 LYFAVYDGHGGPAAADFCFTHMEKICIMDLPLPKKXKLETLTLAFLEIDKAFSSHARLSAD 180
DB 121 LYFAVYDGHGGPAAADFCFTHMEKICIMDLPLPKKXKLETLTLAFLEIDKAFSSHARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVWASVGDSSRAILCRKKGPKMLTIDHTPERKDEKERIKKC 240
DB 181 ATLLTSGTTATVALLRDGIELVWASVGDSSRAILCRKKGPKMLTIDHTPERKDEKERIKKC 240
QY 241 GGFVAMNSLGQPHVNGRLAMTRSGDLDLKTSVGIABPETYKRIKLHHADDSFLVLTDDGI 300
DB 241 GGFVAMNSLGQPHVNGRLAMTRSGDLDLKTSVGIABPETYKRIKLHHADDSFLVLTDDGI 300
QY 301 NFMVNSQEICDFVNOCHDPNEAAHVAITEQAIQYGTEDNSTAVVVPFGAWGKYKNSSEINFS 360
DB 301 NFMVNSQEICDFVNOCHDPNEAAHVAITEQAIQYGTEDNSTAVVVPFGAWGKYKNSSEINFS 360
QY 361 FRSFPASSGRWA 372
DB 361 FRSFPASSGRWA 372

RESULT 13
ADB66824
ID ADB66824 standard; protein; 372 AA.
XX
AC ADB66824;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human PN7740.
XX
KW human; drug candidate screening; neurodegenerative disorder;
KW Huntington's disease; Parkinson's disease; dementia; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN US2002115119-A1.
XX
PD 22-AUG-2002.
XX
PF 10-OCT-2001; 2001US-00973063.
XX
PR 17-OCT-2000; 2000US-0240790P.
XX
PA (MYRI-) MYRIAD GENETICS INC.

XX PI Roch J, Bartel PL, Heichman K;
 XX WPI; 2003-719962/68.
 XX N-PSDB; ADB66827.
 XX
 XX Screening drug candidates for modulating interaction of complexes of
 PT protein, by combining protein in the presence or absence of a drug to
 PT form first and second complex, and measuring and comparing both the
 PT complexes.
 XX
 XX Example 2; Page 22; 36pp; English.
 XX
 XX The invention relates to a method of screening drug candidates for
 CC modulating interaction of proteins in a complex. The method is useful for
 CC screening drug candidates useful in treating neurodegenerative disorder,
 CC by measuring the activity of a protein selected from Mint2 and PDE-9A in
 CC the presence or absence of the drug, and comparing the activity measured,
 CC where if there is a difference in activity, then the drug is a drug
 CC candidate for treating the neurodegenerative disorder. The
 CC neurodegenerative disorder is Huntington's disease. Parkinson's disease,
 CC dementia, or Alzheimer's disease, preferably Alzheimer's disease. The
 CC drug, modulator or compound identified by the methods of the invention
 CC are useful for treating a neurodegenerative disorder. The present
 CC sequence represents the amino acid sequence of human FN7740.
 XX
 XX Sequence 372 AA;
 SQ
 Query Match 100.0%; Score 1951; DB 7; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.5e-206;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSTAALITLVRSNGNQVRRVLLSSRLQLDDRRVPTCHSSTSEPCRSRFPDGGSGSPAT 60
 Db 1 MSTAALITLVRSNGNQVRRVLLSSRLQLDDRRVPTCHSSTSEPCRSRFPDGGSGSPAT 60
 QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIKISLENVGCASQIGKRKENEPRDFQAQLTDEV 120
 Db 61 WDNFGIWDNRIDEPILLPPSIKYGKPIKISLENVGCASQIGKRKENEPRDFQAQLTDEV 120
 QY 121 LYFAVDGCHGGAADPFCHTHMEKCIIMDLKPKEKNETLLTFLAFLEIDKAFSSHARLSAD 180
 Db 121 LYFAVDGCHGGAADPFCHTHMEKCIIMDLKPKEKNETLLTFLAFLEIDKAFSSHARLSAD 180
 QY 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
 Db 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
 QY 241 GGFVANNSLGQPHVNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHHADDSFLVLTDDGI 300
 Db 241 GGFVANNSLGQPHVNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHHADDSFLVLTDDGI 300
 QY 301 NFMVNSQEICDFYNQCHDNEAAHVAITEQAIOYGTEDNSTAVVVPFGAMGKYKNSSEINFS 360
 Db 301 NFMVNSQEICDFYNQCHDNEAAHVAITEQAIOYGTEDNSTAVVVPFGAMGKYKNSSEINFS 360
 QY 361 FSRSPASSGRWA 372
 Db 361 FSRSPASSGRWA 372
 RESULT 14
 ADD73452
 ID ADD73452 standard; protein; 372 AA.
 XX
 XX AC ADD73452;
 XX
 XX DT 29-JAN-2004 (first entry)
 XX
 XX DE Novel human protein FN7740.
 XX
 XX nootropic; neuroprotective; antiparkinsonian; protein binding modulator;
 KW drug screening; neurodegenerative disorder; Huntington's Disease;
 JW

KW Parkinson's Disease; dementia; Alzheimer's Disease; AD; APP; presenilin;
 KW protein-protein interaction; drug target identification; human;
 XX yeast two-hybrid assay; PN7740.
 XX Homo sapiens.
 XX US2003186317-A1.
 XX 02-OCT-2003.
 XX 09-OCT-2001; 2001US-00371782.
 XX 17-OCT-2000; 2000US-0240790P.
 XX (MYRI-) MYRIAD GENETICS INC.
 XX Roch J, Bartel PL, Heichman K;
 XX WPI; 2003-852417/79.
 XX N-PSDB; ADB73455.
 XX In vitro screening for drug useful for treating neurodegenerative
 PT disorder, e.g. Alzheimer's Disease, involves comparing the amount of two
 PT complexes formed from combined proteins of protein complex in the
 PT presence and absence of drug.
 XX
 XX Example 2-33; SEQ ID NO 4; 36pp; English.
 XX
 XX The invention describes screening a drug in vitro by combining proteins
 CC of a protein complex in the presence of a drug to form a first complex;
 CC combining the proteins in the absence of the drug to form a second
 CC complex; measuring the amount of the two complexes; and comparing the
 CC amount of the first complex with the amount of the second complex. The
 CC method is useful for screening drug candidates capable of modulating a
 CC interaction of the proteins of a protein complex, useful for treating a
 CC neurodegenerative disorder, e.g. Huntington's Disease, Parkinson's
 CC Disease, dementia or Alzheimer's Disease (AD). The inventive method
 CC provides for the discovery of additional proteins interacting with
 CC various domains of the major Alzheimer proteins, including APP and the
 CC presenilins. It can also identify the protein-protein interactions that
 CC are involved in Alzheimer's Disease (AD) pathogenesis, and to identify
 CC drug targets. This is the amino acid sequence of a novel human protein
 CC PN7740 identified using yeast two-hybrid assay with a human brain bait
 CC protein.
 XX
 XX Sequence 372 AA;
 SQ

Query Match 100.0%; Score 1951; DB 7; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.5e-206;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSTAALITLVRSNGNQVRRVLLSSRLQLDDRRVPTCHSSTSEPCRSRFPDGGSGSPAT 60
 Db 1 MSTAALITLVRSNGNQVRRVLLSSRLQLDDRRVPTCHSSTSEPCRSRFPDGGSGSPAT 60
 QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIKISLENVGCASQIGKRKENEPRDFQAQLTDEV 120
 Db 61 WDNFGIWDNRIDEPILLPPSIKYGKPIKISLENVGCASQIGKRKENEPRDFQAQLTDEV 120
 QY 121 LYFAVDGCHGGAADPFCHTHMEKCIIMDLKPKEKNETLLTFLAFLEIDKAFSSHARLSAD 180
 Db 121 LYFAVDGCHGGAADPFCHTHMEKCIIMDLKPKEKNETLLTFLAFLEIDKAFSSHARLSAD 180
 QY 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
 Db 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
 QY 241 GGFVANNSLGQPHVNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHHADDSFLVLTDDGI 300
 Db 241 GGFVANNSLGQPHVNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHHADDSFLVLTDDGI 300
 QY 301 NFMVNSQEICDFYNQCHDNEAAHVAITEQAIOYGTEDNSTAVVVPFGAMGKYKNSSEINFS 360
 Db 301 NFMVNSQEICDFYNQCHDNEAAHVAITEQAIOYGTEDNSTAVVVPFGAMGKYKNSSEINFS 360

Db 301 NFMVNSQEICDFVNOCHDPNEAAHVAETEQAIOYGTEDNSTAVVVPFGAMGKYKXNSEINFS 360
 QY 361 FSRSPASSGRWA 372
 Db 361 FSRSPASSGRWA 372

RESULT 15
 ADA54131
 ID ADA54131 standard; protein; 372 AA.
 AC ADA54131;
 XX 20-NOV-2003 (first entry)
 DT Human protein, SEQ ID 1699.
 DE
 DB
 KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
 KW Gene therapy; human; secretory protein; membrane proteins; cancer;
 KW inflammatory disease; osteoporosis; neurological disease.
 XX
 OS Homo sapiens.
 XX
 PN EP1293569-A2.
 PD 19-MAR-2003.
 XX
 PF 21-MAR-2002; 2002EP-00006586.
 XX
 PR 14-SEP-2001; 2001JP-00328381.
 PR 24-JAN-2002; 2002US-0350435P.
 XX
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 DR WPI; 2003-395539/38.
 DR N-ESDB; ADA52492.
 XX
 XX New polynucleotides encoding full-length polypeptides, e.g. secretory
 PT and/or membrane proteins, useful for developing medicines for diseases in
 PT which the gene is involved, or as target molecules for gene therapy.
 PS Claim 14; SEQ ID NO 1699; 205pp; English.
 XX
 CC The present invention relates to novel human secretory or membrane
 CC proteins (ADA54072-ADA5710) and their coding sequences (ADA52433-
 CC ADA54071). The coding sequences are useful in the gene therapy of
 CC diseases caused by abnormalities of the proteins, e.g. cancer,
 CC inflammatory diseases, osteoporosis or neurological disease.
 XX
 SQ Sequence 372 AA;

Query Match 99.9%; Score 1950; DB 6; Length 372;
 Best Local Similarity 99.7%; Pred. No. 2e-206;
 Matches 371; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNQVRRVLLSRLLQDDRRVTPTCHSSTSPRCRFPDGGSGSPAT 60
 Db 1 MSTAALITLVRSQGNQVRRVLLSRLLQDDRRVTPTCHSSTSPRCRFPDGGSGSPAT 60
 QY 61 WDNFGIWNRIDEPILLPPSIKYGKPIPIKISLVNVCASQIGKKNEDRDFDLTLDEV 120
 Db 61 WDNFGIWNRIDEPILLPPSIKYGKPIPIKISLVNVCASQIGKKNEDRDFDLTLDEV 120
 QY 121 LYFAYVDHGGGPAADFCFTHMEKIMDLPPKKNLETLTLTFLAFLEIDKAFSSHARLSAD 180
 Db 121 LYFAYVDHGGGPAADFCFTHMEKIMDLPPKKNLETLTLTFLAFLEIDKAFSSHARLSAD 180
 QY 181 ATLLISGTTATVALLRDGIELVWASVGSRAILCRKGPKMLTIDHTPERKDEKERIKKC 240

Db 181 ATLLISGTTATVALLRDGIELVWASVGSRAILCRKGPKMLTIDHTPERKDEKERIKKC 240
 QY 241 GGFVAVNSLGGPHVNGRLAMTRSIGDLDLKTSGVIAEPETKRIKLHADDGFLVLTDDGI 300
 Db 241 GGFVAVNSLGGPHVNGRLAMTRSIGDLDLKTSGVIAEPETKRIKLHADDGFLVLTDDGI 300
 QY 301 NFMVNSQEICDFVNOCHDPNEAAHVAETEQAIOYGTEDNSTAVVVPFGAMGKYKXNSEINFS 360
 Db 301 NFMVNSQEICDFVNOCHDPNEAAHVAETEQAIOYGTEDNSTAVVVPFGAMGKYKXNSEINFS 360
 QY 361 FSRSPASSGRWA 372
 Db 361 FSRSPASSGRWA 372

RESULT 16
 AAU22934
 ID AAU22934 standard; protein; 373 AA.
 XX AAU22934;
 AC AAU22934;
 XX 18-DEC-2001 (first entry)
 DT Novel human enzyme polypeptide #20.
 DE
 DB
 KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
 KW ligase; hyperproliferative disorder; immunodeficiency disorder;
 KW autoimmune disorder; neurological disorder; metabolic disorder;
 KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
 KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;
 KW nephrotropic; anticoagulant.
 XX
 OS Homo sapiens.
 XX WO200155301-A2.
 XX 02-AUG-2001.
 XX 17-JAN-2001; 2001WO-US0001239.
 XX
 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226868P.
PR 23-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229345P.
PR 01-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 05-SEP-2000; 2000US-0230437P.
PR 05-SEP-2000; 2000US-0230438P.
PR 05-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234233P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234597P.
PR 25-SEP-2000; 2000US-0234598P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0246417P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.

PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 05-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX
XX WPI; 2001-465566/50.
DR N-PSDB; AAS40804.
XX

Novel polypeptides and polynucleotides useful for diagnosing, preventing,

treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.

Claim 11; SEQ ID NO 930; 1180pp; English.

The present invention relates to the isolation of novel human enzyme polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. influenza). The polynucleotides of the invention can also be used in gene therapy. AAU22915-AAU23814 represent the novel human enzyme polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 373 AA;

Query Match 99.4%; Score 1939; DB 4; Length 373;
Best Local Similarity 99.5%; Pred. No. 3.3e-205;
Matches 370; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGVRRVRLSSLLQDDRRVPTCHSSTSEPRCSRFDPDGGSPAT 60
DB 2 MSTAALITLVRSQGVRRVRLSSLLQDDRRVPTCHSSTSEPRCSRFDPDGGSPAT 61

QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRNKEDRDFDFAQLTDEV 120
 Db 62 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRNKEDRDFDFAQLTDEV 121
 QY 121 LYFAVYDGHGGPAAADFCHTHMEKICIMDLLPKKXLETLLTFLAFLEIDKAFSSSHARLSAD 180
 Db 122 LYFAVYDGHGGPAAADFCHTHMEKICIMDLLPKKXLETLLTFLAFLEIDKAFSSSHARLSAD 181
 QY 181 ATLLTSGTTATVALLRGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKK 240
 Db 182 ATLLTSGTTATVALLRGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKK 241
 QY 241 GGFVAMNSLGQPHVNGRLAMTRSGIDLDLKTSGVIAEPETPKRIKLHADDSPFLVLTDDGI 300
 Db 242 GGFVAMNSLGQPHVNGRLAMTRSGIDLDLKTSGVIAEPETPKRIKLHADDSPFLVLTDDGI 301
 QY 301 NFWNSQIEICDFVNOCHDPNEAAHVAHQIYGTEDNSTAVVVPFGANGKYKNSINF 360
 Db 302 NFWNSQIEICDFVNOCHDPNEAAHVAHQIYGTEDNSTAVVVPFGANGKYKNSINF 361
 QY 361 FSRSPASSGRWA 372
 Db 362 FSRSPASSGRWA 373

RESULT 17

AAAB57077
 ID AAB57077 standard; protein; 373 AA.

AC AAB57077;

XX 13-MAR-2001 (first entry)

DE Human prostate cancer antigen protein sequence SEQ ID NO:1655.

XX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
 KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
 KW vulnary; gastrointestinal; nephrotoxic; antineoplastic; gynaecological;
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
 KW wound; infectious disease.

XX Homo sapiens.

XX WO200055174-A1.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US005988.

XX 12-MAR-1999; 99US-0124270P.

 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/); ROSEN C A.

PI Rosen CA, Ruben SM;

XX WPI; 2000-587513/55.

DR N-ESDB; AAF16280.

XX Prostate cancer associated gene sequences, referred to as prostate cancer
 PT antigens, useful for treatment, prevention, and diagnosis of disorders
 PT such as prostate cancer.

XX Claim 11; Page 2113-2114; 2338pp; English.

XX AAF15866 to AAF16505 encode the human prostate cancer associated
 CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
 CC The prostate cancer antigens can have neuroprotective, cytostatic,
 CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,
 CC nephrotoxic, antineoplastic, gynaecological and antibacterial activities,
 CC and can be used in gene therapy. The prostate cancer antigen

CC polynucleotides may be used for detection of prostate cancer, chromosome
 CC identification, as chromosome markers, and for numerous other diagnostic
 CC or research purposes. The prostate cancer antigens may be used to treat
 CC disorders such as neural, immune, muscular, reproductive,
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
 CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
 CC AAB57303 represent sequences used in the exemplification of the present
 CC invention

XX SQ Sequence 373 AA;

Query Match 98.6%; Score 1924; DB 3; Length 373;

Best Local Similarity 98.9%; Pred. No. 1.5e-203;

Matches 368; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSGGNQVRRVLLSRLLQDDRRVPTCHSSTSEPRCSRFPDGGSGPAT 60
 Db 2 MSTAALITLVRSGGNQVRRVLLSRLLQDDRRVPTCHSSTSEPRCSRFPDGGSGPAT 61
 QY 61 WNFNGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRNKEDRDFDFAQLTDEV 120
 Db 62 WNFNGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRNKEDRDFDFAQLTDEV 121
 QY 121 LYFAVYDGHGGPAAADFCHTHMEKICIMDLLPKKXLETLLTFLAFLEIDKAFSSSHARLSAD 180
 Db 122 LYFAVYDGHGGPAAADFCHTHMEKICIMDLLPKKXLETLLTFLAFLEIDKAFSSSHARLSAD 181
 QY 181 ATLLTSGTTATVALLRGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKK 240
 Db 182 ATLLTSGTTATVALLRGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKK 241
 QY 241 GGFVAMNSLGQPHVNGRLAMTRSGIDLDLKTSGVIAEPETPKRIKLHADDSPFLVLTDDGI 300
 Db 242 GGFVAMNSLGQPHVNGRLAMTRSGIDLDLKTSGVIAEPETPKRIKLHADDSPFLVLTDDGI 301
 QY 301 NFWNSQIEICDFVNOCHDPNEAAHVAHQIYGTEDNSTAVVVPFGANGKYKNSINF 360
 Db 302 NFWNSQIEICDFVNOCHDPNEAAHVAHQIYGTEDNSTAVVVPFGANGKYKNSINF 361
 QY 361 FSRSPASSGRWA 372
 Db 362 FSRSPASSGRWA 373

RESULT 18

ABAB07401
 ID ABAB07401 standard; protein; 351 AA.

XX AC ABAB07401;

XX 09-APR-2002 (first entry)

DE Human protein phosphatase IIC ABI2 polypeptide.

XX Protein phosphatase IIC ABI2; antiasthmatic; antiapoptotic; anti-HIV;
 KW neuroprotective; vasotropic; virucide; osteopathic; cytostatic; human;
 KW antiinflammatory; anabolic; cancer.

OS Homo sapiens.

XX WO200196571-A2.

XX 20-DEC-2001.

XX 13-JUN-2001; 2001WO-EP006666.

XX 16-JUN-2000; 2000US-0212043P.

XX 07-AUG-2000; 2000US-0223322P.

XX 13-DEC-2000; 2000US-0254877P.

XX (FARS) BAYER AG.

XX Xiao Y;

XX DR WPI: 2002-139713/18.
 DR N-PSDB; ABA94576.
 XX
 XX Protein phosphatase IIC ABI2 polypeptide and polynucleotides useful for
 PT identifying modulating agents useful in treating diseases e.g. cancer,
 PT inflammatory disorder, osteoporosis, asthma, AIDS and viral infections.
 XX
 XX Claim 26; Fig 18; 135pp; English.
 XX
 XX The invention relates to human protein phosphatase IIC ABI2 polypeptides
 CC and polynucleotides. The polypeptides can be expressed by standard
 CC recombinant methodology. The polypeptides, polynucleotides and modulators
 CC are useful for modulating activity of protein phosphatase IIC ABI2 in a
 CC disease or treating a disease which include asthma, chronic obstructive
 CC pulmonary disease (COPD), peripheral or central nervous system disease
 CC including neurodegenerative disease, a disorder associated with an
 CC increase in apoptosis, including AIDS and other infectious or genetic
 CC immunodeficiency, myelodysplasia, ischemic injury, toxin-induced disease,
 CC wasting disease, viral infection and osteoporosis; or disorder associated
 CC with decrease in apoptosis, including cancer and inflammatory disorder.
 CC Fusion proteins comprising protein phosphatase IIC ABI2 are useful for
 CC generating antibodies and for use in various assay systems, and the
 CC protein phosphatase IIC ABI2 polypeptide can also be used as a bait
 CC protein in a two-hybrid assay or three-hybrid assay. The present sequence
 CC represents a human protein phosphatase IIC ABI2 polypeptide
 XX
 XX Sequence 351 AA;
 SQ
 Query Match 92.7%; Score 1809; DB 5; Length 351;
 Best Local Similarity 100.0%; Pred. No. 7.4e-191;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSTAALITLVRSGGNQVRRVLLSRLLQDDRRVPTCHSSTSEPRCFFPDGSGSPAT 60
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 61 WNFGLWNRIDEPILLPSIKYKPIPKISLVNGCASQIGKRNEDRDFPAQLTDEV 120
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 61 WNFGLWNRIDEPILLPSIKYKPIPKISLVNGCASQIGKRNEDRDFPAQLTDEV 120
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 121 LVFVVDGHHGGAADFCCHTMEKIMDLPPKKNLETLTLTAFLEIDKAFSSHARLSAD 180
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 181 ATLLTSGTTATVALLRDGIELVAVSGDSRAILCRKGRPKLTIDHTPERKDEKERIKKC 240
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 241 GGFVANSIGQHVNGRLAMTSIGDLTKTSGLVABETPKRIKLHHADDSFLVLTDDGI 300
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 301 NFVNSQEICDFVNOCHDPNEAAHVAETQAIQYGTEDNSTAVVVPF 346
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 301 NFVNSQEICDFVNOCHDPNEAAHVAETQAIQYGTEDNSTAVVVPF 346

RESULT 19

ABB78059

ID ABB78059 standard; protein; 352 AA.

XX AC ABB78059;

XX DT 05-NOV-2002 (first entry)

XX DE Amino acid sequence of human 16105 polypeptide.

XX Human; 16105; cancer; cellular proliferation disorder; brain cancer;
 XX cellular differentiation disorder; breast cancer; lung cancer;
 XX ovarian cancer; cardiovascular disorder; hypertension; atherosclerosis;
 XX arrhythmia; heart failure; endothelial cell disorder; psoriasis;
 XX Grave's disease; autoimmune disease; diabetes mellitus; Crohn's disease;

KW viral disease; pain; metabolic disorder.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 26..26
 FT /note= "protein kinase C phosphorylation site"
 FT Modified-site 32..35
 FT /note= "cAMP/cGMP-dependent protein kinase
 FT phosphorylation site"
 FT Modified-site 41..44
 FT /note= "casein kinase II phosphorylation site"
 FT Modified-site 48..51
 FT /note= "casein kinase II phosphorylation site"
 FT Modified-site 56..61
 FT /note= "N-myristoylation site"
 FT Modified-site 65..70
 FT /note= "N-myristoylation site"
 FT Modified-site 80..82
 FT /note= "protein kinase C phosphorylation site"
 FT Modified-site 101..104
 FT /note= "amidation site"
 FT Domain 104..323
 FT /note= "protein phosphatase domain"
 FT Domain 122..130
 FT /note= "protein phosphatase 2C signature"
 FT Modified-site 130..135
 FT /note= "N-myristoylation site"
 FT Modified-site 140..143
 FT /note= "casein kinase II phosphorylation site"
 FT Modified-site 187..192
 FT /note= "N-myristoylation site"
 FT Modified-site 205..208
 FT /note= "casein kinase II phosphorylation site"
 FT Modified-site 241..246
 FT /note= "N-myristoylation site"
 FT Modified-site 263..266
 FT /note= "casein kinase II phosphorylation site"
 FT Modified-site 280..282
 FT /note= "protein kinase C phosphorylation site"
 FT Modified-site 338..341
 FT /note= "casein kinase II phosphorylation site"
 FT Modified-site 338..340
 FT /note= "protein kinase C phosphorylation site"
 XX
 XX US2002077463-A1.
 XX
 XX 20-JUN-2002.
 XX
 XX 17-MAY-2001; 2001US-00860351.
 XX
 XX 19-MAY-2000; 2000US-0205260P.
 XX
 XX (MEYE/) MEYERS R.
 XX
 XX Meyers R;
 XX
 XX WPI: 2002-607448/65.
 XX N-PSDB; ABO78296.
 XX
 XX New polypeptide for treating a subject having a disorder or at risk of
 XX developing a proliferative disorder, cardiovascular disorder, autoimmune
 XX or metabolic disorder.
 XX
 XX Claim 4; Fig 1a-b; 50pp; English.
 XX
 XX The present sequence represents a human polypeptide, designated 16105.
 XX 16105 polypeptides and polynucleotides are used for evaluating the
 XX efficacy of a treatment of cancer or a cellular proliferation and/or
 XX differentiation disorder in a subject. They are also useful for
 XX diagnosing a cancer or a cellular proliferation and/or differentiation
 XX disorder in a subject. The cancer or cellular proliferation and/or
 XX differentiation is breast, lung, brain or ovarian cancer. They may also

CC be used for treating proliferative disorders e.g., cancer; cardiovascular
CC disorders e.g., hypertension, atherosclerosis, arrhythmias, heart failure
CC ; endothelial cell disorders e.g., psoriasis, Grave's disease; autoimmune
CC diseases e.g., diabetes mellitus, Crohn's disease; viral diseases; pain;
CC or metabolic disorders
XX
SQ Sequence 352 AA;

Query Match 88.5%; Score 1727; DB 5; Length 352;
Best Local Similarity 99.4%; Pred. No. 8.9e-182;
Matches 330; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSTAAALTLVRSGNQVRRVLLSSRLQLQDDRRVPTCHSTSEPRCSRFPDGGSPAT 60
Db 1 MSTAAALTLVRSGNQVRRVLLSSRLQLQDDRRVPTCHSTSEPRCSRFPDGGSPAT 60
Qy 61 WDNFGIWNDRIDEPIILLPSIKYKGPPIKISLENVGCASOIGRKENEDRFPDQAULTDEV 120
Db 61 WDNFGIWNDRIDEPIILLPSIKYKGPPIKISLENVGCASOIGRKENEDRFPDQAULTDEV 120
Qy 121 LYFVYDGHGGPAAADFCHTHMEKIMDLPLKKNLETLTLTAFLEIDKAFSSHARLSAD 180
Db 121 LYFVYDGHGGPAAADFCHTHMEKIMDLPLKKNLETLTLTAFLEIDKAFSSHARLSAD 180
Qy 181 ATLLTSGTTATVALLRGGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
Db 181 ATLLTSGTTATVALLRGGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
Qy 241 GGFVAMNSLQGVHNGRLAMTRISGDLDLKTSGVIAEPETKRIKLHADDSEFLVLTDDGI 300
Db 241 GGFVAMNSLQGVHNGRLAMTRISGDLDLKTSGVIAEPETKRIKLHADDSEFLVLTDDGI 300
Qy 301 NFMVNSQIEICDFVNQCHDPNEAAHVAETEQAIIQ 332
Db 301 NFMVNSQIEICDFVNQCHDPNEAAHVAETEQAIIQ 332

RESULT 20
ADE31687
ID ADE31687 standard; protein; 352 AA.
XX ADE31687;
AC ADE31687;
XX
DT 29-JAN-2004 (first entry)
XX
XX Human 16105 protein #SEQ ID 44.

XX Antiatherosclerotic; cardiant; vasotropic; antiinflammatory;
XX thrombolytic; antiarrhythmic; antianginal; hypotensive; gene therapy;
XX cardiovascular; disorder; ischaemia; aortic bending;
XX vascular heart disease; endocarditis; atrial fibrillation; heart failure;
XX angina; cardiomyopathy; cardiac death.

XX Homo sapiens.
XX WO2003065984-A2.
XX
XX 14-AUG-2003.
XX
XX 29-JAN-2003; 2003WO-US002571.
XX
XX 01-FEB-2002; 2002US-0353224P.
XX 15-MAR-2002; 2002US-0364529P.
XX 19-APR-2002; 2002US-0373861P.
XX 29-APR-2002; 2002US-0376287P.
XX 12-JUN-2002; 2002US-0388080P.
XX 24-JUN-2002; 2002US-0390971P.
XX 03-JUL-2002; 2002US-0394130P.
XX 10-JUL-2002; 2002US-0394797P.
XX 21-AUG-2002; 2002US-0404904P.
XX 23-AUG-2002; 2002US-0405450P.
XX 04-SEP-2002; 2002US-0408070P.
XX 06-NOV-2002; 2002US-0424300P.

PR 05-DEC-2002; 2002US-0431042P.
PR 05-DEC-2002; 2002US-0431079P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Logan TU, Chun M, Galvin KM, Healy A, Acton SL, Donaghue M;
XX Stagliano N, Perodin J, Rodrigue-Way A;
XX
XX WPI; 2003-731468/69.
XX N-PSDB; ADE31686.

XX Identifying a compound capable of treating a cardiovascular disorder
XX (e.g. atherosclerosis) comprises assaying the ability of the compound to
XX modulate the expression or activity of e.g. 1682, 6169 or 6193
XX polypeptide or nucleic acid.
XX
XX Disclosure; SEQ ID NO 44; 328pp; English.

XX The invention relates to a method for identifying a compound capable of
XX treating a cardiovascular disorder. The present invention identifies the
XX differential expression of 1682, 6169, 6193, 7771, 14395, 28002, 33216,
XX 43726, 69292, 21656, 32427, 2402, 7747, 1720, 9151, 60491, 1371, 7077,
XX 33207, 1419, 18036, 16105, 38650, 14245, 58548, 1870, 25856, 32394, 3484,
XX 345, 9252, 9135, 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912,
XX 2868, 283, 2534, 9464, 17799, 26686, 43948, 32135, 12208, 2914, 51130,
XX 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474, 9792, 15400, 1452 or
XX 6585 genes in cardiovascular disease states. The methods are useful in
XX diagnosing, preventing and treating cardiovascular disorders, such as
XX atherosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury,
XX restenosis, arterial inflammation, vascular wall remodeling, coronary
XX microembolism, tachycardia, bradycardia, pressure overload, aortic
XX bending, coronary artery ligation, vascular heart disease, valvular
XX disease, including but not limited to, valvular degeneration caused by
XX calcification, rheumatic heart disease, endocarditis, or complications of
XX artificial valves; atrial fibrillation, long-QT syndrome, congestive
XX heart failure, sinus node dysfunction, angina, heart failure,
XX hypertension, atrial fibrillation, atrial flutter, pericardial disease,
XX including but not limited to, pericardial effusion and pericarditis;
XX cardiomyopathies, e.g. dilated cardiomyopathy or idiopathic
XX cardiomyopathy, myocardial infarction, coronary artery disease, coronary
XX artery spasm, ischaemic disease, arrhythmia, sudden cardiac death and
XX cardiovascular developmental disorders. The methods may also be used for
XX identifying compounds that modulate cardiovascular disorders. Sequences
XX given in ADE31644-ADE31769 represent the genes and proteins that may be
XX regulated by a compound of the invention.

XX Sequence 352 AA;
XX
XX Query Match 88.5%; Score 1727; DB 7; Length 352;
XX Best Local Similarity 99.4%; Pred. No. 8.9e-182;
XX Matches 330; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSTAAALTLVRSGNQVRRVLLSSRLQLQDDRRVPTCHSTSEPRCSRFPDGGSPAT 60
Db 1 MSTAAALTLVRSGNQVRRVLLSSRLQLQDDRRVPTCHSTSEPRCSRFPDGGSPAT 60
Qy 61 WDNFGIWNDRIDEPIILLPSIKYKGPPIKISLENVGCASOIGRKENEDRFPDQAULTDEV 120
Db 61 WDNFGIWNDRIDEPIILLPSIKYKGPPIKISLENVGCASOIGRKENEDRFPDQAULTDEV 120
Qy 121 LYFVYDGHGGPAAADFCHTHMEKIMDLPLKKNLETLTLTAFLEIDKAFSSHARLSAD 180
Db 121 LYFVYDGHGGPAAADFCHTHMEKIMDLPLKKNLETLTLTAFLEIDKAFSSHARLSAD 180
Qy 181 ATLLTSGTTATVALLRGGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
Db 181 ATLLTSGTTATVALLRGGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
Qy 241 GGFVAMNSLQGVHNGRLAMTRISGDLDLKTSGVIAEPETKRIKLHADDSEFLVLTDDGI 300
Db 241 GGFVAMNSLQGVHNGRLAMTRISGDLDLKTSGVIAEPETKRIKLHADDSEFLVLTDDGI 300
Qy 301 NFMVNSQIEICDFVNQCHDPNEAAHVAETEQAIIQ 332

DB 301 NFMVNSQICDFVNOCHDPNEAAHVTEQVTQ 332

RESULT 21

ABBO7392
ID ABB07392 standard; protein; 373 AA.
XX
AC ABB07392;
XX
DT 09-APR-2002 (first entry)
XX
DE Human protein phosphatase IIC ABI2 polypeptide.
XX
KW Protein phosphatase IIC ABI2; antiasthmatic; antiapoptotic; anti-HIV;
KW neuroprotective; vasotropic; virucide; osteopathic; cytostatic; human;
KW antiinflammatory; anabolic; cancer.
XX
OS Homo sapiens.
XX
FN WO2001196571-A2.
XX
PD 20-DEC-2001.
XX
PF 13-JUN-2001; 2001WO-EP006666.
XX
PR 16-JUN-2000; 2000US-0212043P.
PR 07-AUG-2000; 2000US-0223322P.
PR 13-DEC-2000; 2000US-0254877P.
XX
PA (PARB) BAYER AG.
XX
PI Xiao Y;
XX
XX WPI; 2002-139713/18.
DR N-PSDB; ABA94569.
XX

Protein phosphatase IIC ABI2 polypeptide and polynucleotides useful for identifying modulating agents useful in treating diseases e.g. cancer, inflammatory disorder, osteoporosis, asthma, AIDS and viral infections.
Claim 26; Fig 2; 135pp; English.

The invention relates to human protein phosphatase IIC ABI2 polypeptides and polynucleotides. The polypeptides can be expressed by standard recombinant methodology. The polypeptides, polynucleotides and modulators are useful for modulating activity of protein phosphatase IIC ABI2 in a disease or treating a disease which include asthma, chronic obstructive pulmonary disease (COPD), peripheral or central nervous system disease including neurodegenerative disease, a disorder associated with an increase in apoptosis, including AIDS and other infectious or genetic immunodeficiency, myelodysplasia, ischemic injury, toxin-induced disease, wasting disease, viral infection and osteoporosis; or disorder associated with decrease in apoptosis, including cancer and inflammatory disorder. Fusion proteins comprising protein phosphatase IIC ABI2 are useful for generating antibodies and for use in various assay systems, and the protein phosphatase IIC ABI2 polypeptide can also be used as a bait protein in a two-hybrid assay or three-hybrid assay. The present sequence represents a human protein phosphatase IIC ABI2 polypeptide

Sequence 373 AA;

Query Match 78.9%; Score 1538.5; DB 5; Length 373;
Best Local Similarity 85.6%; Pred. No. 7.3e-161;
Matches 303; Conservative 6; Mismatches 22; Indels 23; Gaps 3;

QY 1 MSTAALITLVRSQGVNRVLLSRLQDDRRVPTCHSTSEPRCSRFPDGGSGPAT 60
DB 1 MSTAALITLVRSQGVNRVRLSRLQDDRRVPTCHSTSEPRCSRFPDGGSGPAT 60
QY 61 WDNFGIWNDRIDEPILLPSIKYGRPIPKISLENVGCASQIGKRKENEEDRFDFAQLTDEV 120
DB 61 WDNFGIWNDRIDEPILLPSIKYGRPIPKISLENVGCASQIGKRKENEEDRFDFAQLTDEV 120

QY 121 LYFAVDYDGHGGPAAADFCHTHMEKCMIDLPLKPKNLETLTLTFLAFLEI----DKAFSSSHAR 176
DB 121 LYFAVDYDGHGGPAAADFCHTHMEKCMFYM-PEHNSWVKFVFASVRVICGRELCLVSSSR 179
QY 177 LSA-----DATLITSGTTATVALLRDGIELVVASVGDRAILCKGK 218
DB 180 PGARGHYMRGFGSKRDLLNFVPATLITSGTTATVALLRDGIELVVASVGDRAILCKGK 239
QY 219 PMKLITIDHTPERKDEKERIKKCGGFVAVNSLGGPHVNGRLAMTRSICDLDLKTSGVIAEP 278
DB 240 PMKLITIDHTPERKDEKERIKKCGGFVAVNSLGGPHVNGRLAMTRSICDLDLKTSGVIAEP 299
QY 279 ETKRIKLHADDGFLVLTDTGINFVMSQICDFVNOCHDPNEAAHVTEQAIQ 332
DB 300 ETKRIKLHADDGFLVLTDTGINFVMSQICDFVNOCHDPNEAAHVTEQVTQ 353

RESULT 22

ABG06716
ID ABG06716 standard; protein; 1072 AA.
XX
AC ABG06716;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #6707.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
FN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.

Drmanac RT, Liu C, Tang YT;
WPI; 2001-639362/73.
N-PSDB; AAS70903.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 20; SEQ ID NO 37075; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic

CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1072 AA;

Query Match	70.5%; Score 1375.5; DB 4; Length 1072;
Best Local Similarity	46.5%; Pred. No. 4.6e-142;
Matches 302; Conservative	6; Mismatches 20; Indels 321; Gaps 4;
QY	Ddb
1	MSTAALITLVRSGNQVRRRLSSRLLODDRVTPTCHSSTSEPRCSRFDPDGSGSPAT 60
1	MSTAALITLVRSGNQVRRRLSSRLLODDRVTPTCHSSTSEPRCSRFDPDGSGSPAT 50
61	WNFGIWNRIDEPILLPPSIKYKPIPKISLVNVCASQIGKRKENEDRFPAQLTDSV 120
61	WNFGIWNRIDEPILLPPSIKYKPIPKISLVNVCASQIGKRKENEDRFPAQLTDSV 120
121	LYFAYVDGHGGPAAADFCHTHMEKICIMDLPEKNLETLTLTAFLFI-----DKATSSHAR 176
121	LYFAYVDGHGGPAAADFCHTHMEKICIMFVN--FEHNSWVFVFASVRVICGRECLVLSSSR 179
177	LSA-----DATTLSGTTATVALLRDGIELVVASVGDSRAILCRKGK 218
180	PGARGHYRMFGSKRDLLNFVPATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGK 239
219	PMKLTIIDHTPERKDKERIKKCGGFVAWNSIQPHVNGPLAMTRSGIDLTKTSGVIAEP 278
240	PMKLTIIDHTPERKDKERIKKCGGFVAWNSIQPHVNGPLAMTRSGIDLTKTSGVIAEP 299
279	ETKRIK-----284
300	ETKRIKLWNSPCGMVLLFFLTCTQSASITCTQSCSITCTQSSSITCTQSASPASNQPASP 359
285	-----284
360	APKQSPASPSPQSPAPNPQASPPTPNQPASSAPNPQSPAPNPQASLAPNPASSAPNPQ 419
285	-----284
420	PASPAPNPQSPAPNPQHHLHPISITCTQSPASSOPASPAPNPQSPAPNPQHHLHPISI 479
285	-----284
480	TCTQSAAPASPAPNPQHHLHTASIITCTQSANITCTQSANIACQTQSSSITCTQSSI 539
285	-----284
540	TCTQASITCISASITCTQSPASPAPNPQTPAPNPQSPAPNPQSPAPNPQHHLHPISOH 599
285	----LHHADDSFLVLTDDGINFWNSQEICDFVNOCHDNFAAHAVTEQ 329
600	HLLHPLFHADDNFLVLTDDGINFWNSQEICDFVNOCHDNFAAHAVTEQ 648
RESULT 23	
ID	ABG28412
XX	ABG28412 standard; protein; 1195 AA.
XX	ABG28412;
XX	DT 18-FEB-2002 (first entry)
XX	Novel human diagnostic protein #28403.
XX	DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX	KW food supplement; medical imaging; diagnostic; genetic disorder.
XX	OS Homo sapiens.
XX	PN WO200175067-A2.
XX	XX

11-OCT-2001.

30-MAR-2001; 2001WO-US0008631.

31-MAR-2000; 2000US-00540217.

23-AUG-2000; 2000US-00649167.

(HYSE-) HYSEQ INC.

Drmanac RT, Liu C, Tang YT;
WPI; 2001-639362/73.
N-PSDB; AAS92599.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 20; SEQ ID NO 58771; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences. The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

Sequence 1195 AA;

```

Query Match      70.5%; Score 1375.5; DB 4; Length 1195;
Best Local Similarity 46.5%; Pred. No. 5.5e-142;
Matches 302; Conservative 6; Mismatches 20; Indels 321; Gaps 4;

1  MSTAALITLYRSGGNQYRRVLLSSRLLODRRVYPTCHSSTSPCSRFPDGGSGSPAT 60
|||||
1  MSTAALITLYRSGGNQYRRVLLSSRLLODRRVYPTCHSSTSPCSRFPDGGSGSPAT 60
|||||

61  WDNFGIWDNRIDRPIILLPPSIKYGKPIPKISLENVGCASOIGKKEKEDRDFDQLTDEV 120
|||||
61  WDNFGIWDNRIDRPIILLPPSIKYGKPIPKISLENVGCASOIGKKEKEDRDFDQLTDEV 120
|||||

121 LYFAVYDGHGGPAAADFCHTHMEKCIMDLAPKPKENLETLLTFLAEI-----DKAFSSHAR 176
|||||
121 LYFAVYDGHGGPAAADFCHTHMEKCIMFVM-FEHSVMVKFVFSRVICGRELCLVSSSR 179
|||||

177 LSA-----DATTLLSGTWTATVALLRDGIELVWVSGDSRAILCRKGK 218
|||||
180 PGARGHYMRGFSGKRDLNLFVPATLLTSGTATVALLRDGIELVWVSGDSRAILCRKGK 239
|||||

219 PMKLTIDHTPERKDEKERIKKCGGFVWNSLQPHVNGRLAMTRESIGDLDLKTSGVIAEP 278
|||||
240 PMKLTIDHTPERKDEKERIKKCGGFVWNSLQPHVNGRLAMTRESIGDLDLKTSGVIAEP 299
|||||

279 ETKRIK-----DATTLLSGTWTATVALLRDGIELVWVSGDSRAILCRKGK 284
|||||
300 ETKRIKWNSEPGEMVLLFFITCTQASITCTQSSITCTQSSITCTQSSASPASNQPASP 359
|||||

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QY 285 ----- 284
 DB 360 APKQSPAPSPAPNPQSPPTNPQSPAPNPQSPAPNPQSPAPNPQ 419
 QY 285 ----- 284
 DB 420 PASPAPNPQSPAPNPQHLLPISITQSPASPQSPAPNPQSPAPNPQHLLPISI 479
 QY 285 ----- 284
 DB 480 TCTQSAAPSPAPNPQSPAPNPQHLLPISITQSANITQSANITQSSITCTQSSSI 539
 QY 285 ----- 284
 DB 540 TCTQSAITCISASITCTQSPASPAPNPQLTPAPNPQSPAPNPQSPAPNPQHLLPISQH 599
 QY 285 -----LHHADDSFLVLTDDGTFNFWNSQEIICDFVNOCHDPNEAAHVTQ 329
 DB 600 HLHPLHADDLSFLVLTDDGTFNFWNSQEIICDFVNOCHDPNEAAHVTQ 648

 RESULT 24
 AAM41604
 ID AAM41604 standard; protein; 238 AA.
 AC AAM41604;
 DT 22-OCT-2001 (first entry)
 DE Human polypeptide SEQ ID NO 6535.
 KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 OS Homo sapiens.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PF 26-DEC-2000; 2000WO-US034263.
 PR 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-00552317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00620312.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 PA (HYSE-) HYSEQ INC.
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Drmanac RT;
 DR WPI: 2001-442253/47.
 DR N-PSDB; AAI60760.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.
 XX
 PS Example 2; SEQ ID NO 6535; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
 CC encoded polypeptides (AAM38642-AAW42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful

CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemia and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification
 XX
 SQ Sequence 238 AA;
 Query Match 58.9%; Score 1150; DB 4; Length 238;
 Best Local Similarity 99.6%; Pred. No. 3.7e-118;
 Matches 224; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 148 DLLPKKNLETLTLTFLAFLIDKAFSSHARLSADATLLTSGTTATVALLRDGIELVVASVG 207
 DB 14 DLLPKKNLETLTLTFLAFLIDKAFSSHARLSADATLLTSGTTATVALLRDGIELVVASVG 73
 QY 208 DSRAILCRKGKPKMLTIDHTPERKDEKERIKKGGFVAVNSLQOPHVNGLAMTRISIGDL 267
 DB 74 DSRAILCRKGKPKMLTIDHTPERKDEKERIKKGGFVAVNSLQOPHVNGLAMTRISIGDL 133
 QY 268 DLKTSVIAPEPTKRIKLHADDLSFLVLTDDGTFNFWNSQEIICDFVNOCHDPNEAAHVT 327
 DB 134 DLKTSVIAPEPTKRIKLHADDLSFLVLTDDGTFNFWNSQEIICDFVNOCHDPNEAAHVT 193
 QY 328 EQAIQYGTEDNSTAVVVPFGANGKYKNSINFSPSSPASSGRWA 372
 DB 194 EQAIQYGTEDNSTAVVVPFGANGKYKNSINFSPSSPASSGRWA 238
 RESULT 25
 AAB47431
 ID AAB47431 standard; protein; 233 AA.
 AC AAB47431;
 DT 31-OCT-2001 (first entry)
 DE Human protein phosphatase 2C26.
 KW Human; protein phosphatase 2C26; diagnosis; malignant tumor; hemopathy;
 KW human immunodeficiency virus; HIV; inflammation.
 OS Homo sapiens.
 XX WO200155425-A1.
 PN 02-AUG-2001.
 PD 15-JAN-2001; 2001WO-CN000054.
 PF 26-JAN-2000; 2000CN-00111524.
 PR (BIOD-) BIODOR GENE TECHNOLOGY LTD SHANGHAI.
 PI Mac Y, Xie Y;
 DR WPI: 2001-483265/52.
 DR N-PSDB; AAH43207.
 XX Human protein phosphatase 2C26 and encoded polynucleotide, used in
 XX diagnosis and treatment of malignant tumors, hemopathy, human
 XX immunodeficiency virus infection, immunological diseases and
 XX inflammation.
 XX Claim 1; Page 27; 33pp; Chinese.

CC This sequence shows human protein phosphatase 2C26. The polypeptide and
CC encoded polynucleotide may be used in diagnosis and treatment of
CC malignant tumors, hemopathy, human immunodeficiency virus (HIV)
CC infection, immunological diseases and inflammation
XX
XX
SQ Sequence 233 AA;

Query Match 48.8%; Score 951.5; DB 4; Length 233;
Best Local Similarity 86.6%; Pred. No. 3.4e-96;
Matches 187; Conservative 5; Mismatches 17; Indels 7; Gaps 1;

Qy 1 MSTAALITLVRSQGNQVRRVLLSSRLQLQDRRTPTCHSSTSEPRCSRDPDQSGSPAT 60
Db 1 MSTAALITLVRSQGNQVRRVLLSSRLQLQDRRTPTCHSSTSEPRCSRDPDQSGSPAT 60

Qy 61 WDNFGIWNRIIDEPILLPPSIKYKPKISLENVGCASQIGRKENEDRFDPAQLTDEV 120
Db 61 WDNFGIWNRIIDEPILLPPSIKYKPKISLENVGCASQIGRKENEDRFDPAQLTDEV 120

Qy 121 LYFAVYDGHGGPAAADFCHTHMEKIMDLLPKENKLETLTLTFLAFLDKAFSSHARLSAD 180
Db 121 LYFAVYDGHGGPAAADFCHTHMEKIMDLLPKENKLETLTLTFLAFLDKAFSSHARLSAD 180

Qy 181 ATLLTSGT-----TATVALLRDIIELVASVGDS 209
Db 181 ENCAWSAALDLEPVDITCGASVEREICLLSQVKES 216

RESULT 26
AAM39818
ID AAM39818 standard; protein; 153 AA.
AC
AC AAM39818;
XX
XX
XX 22-OCT-2001 (first entry)
XX
XX Human polypeptide SEQ ID NO 2963.
XX
XX Homo sapiens.
XX OS
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US034263.
XX
XX 23-DEC-1999; 99US-00471275.
XX 21-JAN-2000; 2000US-00488725.
XX 25-APR-2000; 2000US-00552317.
XX 20-JUN-2000; 2000US-00598042.
XX 19-JUL-2000; 2000US-00620312.
XX 03-AUG-2000; 2000US-00653450.
XX 14-SEP-2000; 2000US-00662191.
XX 19-OCT-2000; 2000US-00693036.
XX 29-NOV-2000; 2000US-00727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
XX Zhou P, Goodrich R, Drmanac RT;
XX WPI; 2001-442253/47.
XX N-PSDB; AAI58974.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such

PT as central nervous system injuries.
XX
XX Example 4; SEQ ID NO 2963; 10078bp; English.
XX
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM39642-AAM42213) with nootropic, and the
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
XX Sequence 153 AA;
SQ

Query Match 41.7%; Score 814; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 2.9e-81;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 220 MKLTIDHTPERDEKERIKKCGFVAMNSLGGPHVNGSLAMTRSIGDLDLKTSGVIAEPE 279
Db 1 MKLTIDHTPERDEKERIKKCGFVAMNSLGGPHVNGSLAMTRSIGDLDLKTSGVIAEPE 60

Qy 280 TKRIKLHADDSEFLVLTDDGTFNFMVNSQIEICDFVNQCHDPNEAAHVAHQIYQTEDNS 339
Db 61 TKRIKLHADDSEFLVLTDDGTFNFMVNSQIEICDFVNQCHDPNEAAHVAHQIYQTEDNS 120

Qy 340 TAVVYVPGNGWKYKNSINFESRSFASGGWA 372
Db 121 TAVVYVPGNGWKYKNSINFESRSFASGGWA 153

RESULT 27
ADA55670
ID ADA55670 standard; protein; 150 AA.
XX
XX ADA55670;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human protein, SEQ ID 3238.
XX
XX Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
XX Gene Therapy; human; secretory protein; membrane proteins; cancer;
XX inflammatory disease; osteoporosis; neurological disease.
XX
XX Homo sapiens.
XX
XX EP1293569-A2.
XX
XX 19-MAR-2003.
XX
XX 21-MAR-2002; 2002EP-00006586.
XX
XX 14-SEP-2001; 2001JP-00328381.
XX 24-JAN-2002; 2002US-0350435P.
XX
XX (HELI-) HELIX RES INST.
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Iehli S;
XX Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
XX Seki N, Yoshikawa I, Otsuka M, Nagahari K, Masuho Y;
XX WPI; 2003-395539/38.
XX N-PSDB; ADA54031.
XX
XX

XX New polynucleotides encoding full-length polypeptides, e.g. secretory
PT and/or membrane proteins, useful for developing medicines for diseases in
PT which the gene is involved, or as target molecules for gene therapy.
XX
PS Claim 14; SEQ ID NO 3238; 205pp; English.
XX
CC The present invention relates to novel human secretory or membrane
CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
CC ADA54071). The coding sequences are useful in the gene therapy of
CC diseases caused by abnormalities of the proteins, e.g. cancer,
CC inflammatory diseases, osteoporosis or neurological disease.
XX
SQ Sequence 150 AA;
Query Match 40.5%; Score 790; DB 6; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.3e-78;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSTAALITLVRSNGNVRRLVLLSRLQDDRRVTPTCHSSTSEPRCSRFPDGGSGPAT 60
DB 1 MSTAALITLVRSNGNVRRLVLLSRLQDDRRVTPTCHSSTSEPRCSRFPDGGSGPAT 60
QY 61 WDNFGIWNRIDEPILLPSIKYKPIPKISLENVGCASQIGKRKENEEDRFDFALITDEV 120
DB 61 WDNFGIWNRIDEPILLPSIKYKPIPKISLENVGCASQIGKRKENEEDRFDFALITDEV 120
QY 121 LYFVAVYDGHGGAADFCFTHMEKICIM 147
DB 121 LYFVAVYDGHGGAADFCFTHMEKICIM 147
RESULT 28
ABB07393
ID ABB07393 standard; protein; 156 AA.
AC ABB07393;
XX
DT 09-APR-2002 (first entry)
DE Human protein phosphatase IIC ABI2 polypeptide.
XX
KW Protein phosphatase IIC ABI2; antiasthmatic; antiapoptotic; anti-HIV;
KW neuroprotective; vasotropic; virucide; osteopathic; cytostatic; human;
KW antiinflammatory; anabolic; cancer.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 2 /note= "encoded by CAN"
FT FT
FT Misc-difference 9 /note= "encoded by TGA"
FT FT
FT Misc-difference 14 /note= "encoded by A"
FT FT
XX WO200196571-A2.
XX
PD 20-DEC-2001.
XX
XX 13-JUN-2001; 2001WO-EP006666.
XX
XX 16-JUN-2000; 2000US-0212043P.
PR 07-AUG-2000; 2000US-0223322P.
PR 13-DEC-2000; 2000US-0254877P.
XX
XX (FARB) BAYER AG.
XX
XX Xiao Y;
XX
XX WPI; 2002-139713/18.
DR N-PSDB; ABA94570.
XX

PT Protein phosphatase IIC ABI2 polypeptide and polynucleotides useful for
PT identifying modulating agents useful in treating diseases e.g. cancer,
PT inflammatory disorder, osteoporosis, asthma, AIDS and viral infections.
XX
PS Claim 37; Fig 4; 135pp; English.
XX
CC The invention relates to human protein phosphatase IIC ABI2 polypeptides
CC and polynucleotides. The polypeptides can be expressed by standard
CC recombinant methodology. The polypeptides, polynucleotides and modulators
CC are useful for modulating activity of protein phosphatase IIC ABI2 in a
CC disease or treating a disease which include asthma, chronic obstructive
CC pulmonary disease (COPD), peripheral or central nervous system disease
CC including neurodegenerative disease, a disorder associated with an
CC increase in apoptosis, including AIDS and other infectious or genetic
CC immunodeficiency, myelodysplasia, ischemic injury, toxin-induced disease,
CC wasting disease, viral infection and osteoporosis; or disorder associated
CC with decrease in apoptosis, including cancer and inflammatory disorder.
CC Fusion proteins comprising protein phosphatase IIC ABI2 are useful for
CC generating antibodies and for use in various assay systems, and the
CC protein phosphatase IIC ABI2 polypeptide can also be used as a bait
CC protein in a two-hybrid assay or three-hybrid assay. The present sequence
CC represents a human protein phosphatase IIC ABI2 polypeptide
XX
SQ Sequence 156 AA;
Query Match 34.3%; Score 669.5; DB 5; Length 156;
Best Local Similarity 95.7%; Pred. No. 3e-65;
Matches 132; Conservative 1; Mismatches 4; Indels 1; Gaps 1;
QY 182 TLLTSGTTATVALLRGIELVWASVGDSEAILCRKPKMKLTIDHTPERKDKERIKKCG 241
DB 19 TLLTSGTTATVALLRGIELVWASVGDSEAILCRKPKMKLTIDHTPERKDKERIKKCG 78
QY 242 GFVAVNSL-GQPHVNGRLAWTRSIGDLTKTSGVIAEPETKIKLHHADDSFLVLTDDGI 300
DB 79 GFVAVNSL-GQPHVNGRLAWTRSIGDLTKTSGVIAEPETKIKLHHADDSFLVLTDDGI 138
QY 301 NFMVNSQEICDFVNQCHD 318
DB 139 NFMVNSQEICDFVNQCHD 156
RESULT 29
ABB07397
ID ABB07397 standard; protein; 83 AA.
AC ABB07397;
XX
DT 09-APR-2002 (first entry)
DE Human protein phosphatase IIC ABI2 polypeptide.
XX
KW Protein phosphatase IIC ABI2; antiasthmatic; antiapoptotic; anti-HIV;
KW neuroprotective; vasotropic; virucide; osteopathic; cytostatic; human;
KW antiinflammatory; anabolic; cancer.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 72 /note= "encoded by ANC"
FT FT
FT FT
XX WO200196571-A2.
XX
PD 20-DEC-2001.
XX
XX 13-JUN-2001; 2001WO-EP006666.
XX
XX 16-JUN-2000; 2000US-0212043P.
PR 07-AUG-2000; 2000US-0223322P.
PR 13-DEC-2000; 2000US-0254877P.
XX
XX (FARB) BAYER AG.
XX

XX Xiao Y;
 PI WPI: 2002-139713/18.
 DR N-PSDB; ABA94574.
 XX
 PT Protein phosphatase IIC ABI2 polypeptide and polynucleotides useful for
 PT identifying modulating agents useful in treating diseases e.g. cancer,
 PT inflammatory disorder, osteoporosis, asthma, AIDS and viral infections.
 XX
 XX Claim 37; Fig 12; 135pp; English.
 PS
 PS The invention relates to human protein phosphatase IIC ABI2 polypeptides
 CC and polynucleotides. The polypeptides can be expressed by standard
 CC recombinant methodology. The polypeptides, polynucleotides and modulators
 CC are useful for modulating activity of protein phosphatase IIC ABI2 in a
 CC disease or treating a disease which include asthma, chronic obstructive
 CC pulmonary disease (COPD), peripheral or central nervous system disease
 CC including neurodegenerative disease, a disorder associated with an
 CC increase in apoptosis, including AIDS and other infectious or genetic
 CC immunodeficiency, myelodysplasia, ischemic injury, toxin-induced disease,
 CC wasting disease, viral infection and osteoporosis; or disorder associated
 CC with decrease in apoptosis, including cancer and inflammatory disorder.
 CC Fusion proteins comprising protein phosphatase IIC ABI2 are useful for
 CC generating antibodies and for use in various assay systems, and the
 CC protein phosphatase IIC ABI2 polypeptide can also be used as a bait
 CC protein in a two-hybrid assay or three-hybrid assay. The present sequence
 CC represents a human protein phosphatase IIC ABI2 polypeptide
 XX
 SQ Sequence 83 AA;
 Query Match 22.4%; Score 437; DB 5; Length 83;
 Best Local Similarity 98.8%; Pred. No. 6e-40;
 Matches 82; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 283 IKLHADSFLVLTGDFNFMVNSQEICDFVNCQCHDPNEAAHVAETQAIQYGTEDNSTAV 342
 Db 1 IKLHADSFLVLTGDFNFMVNSQEICDFVNCQCHDPNEAAHVAETQAIQYGTEDNSTAV 60
 QY 343 VVPGGAWGKYKXSEINFSSRSF 365
 Db 61 VVPGGAWGKYKXSEINFSSRSF 83
 RESULT 30
 AAG06997
 ID AAG06997 standard; protein; 354 AA.
 XX
 AC AAG06997;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 3980.
 XX
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX
 OS Arabidopsis thaliana.
 XX
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 25-FEB-2000; 2000EP-00301439.
 XX
 PR 25-FEB-1999; 99US-0121825P.
 PR 05-MAR-1999; 99US-0123180P.
 PR 09-MAR-1999; 99US-0123548P.
 PR 23-MAR-1999; 99US-0125788P.
 PR 25-MAR-1999; 99US-0126264P.
 PR 29-MAR-1999; 99US-0126785P.
 PR 01-APR-1999; 99US-0127462P.

06-APR-1999; 99US-0128234P.
 08-APR-1999; 99US-0128714P.
 16-APR-1999; 99US-0129845P.
 19-APR-1999; 99US-0130077P.
 21-APR-1999; 99US-0130449P.
 23-APR-1999; 99US-0130510P.
 28-APR-1999; 99US-0130891P.
 30-APR-1999; 99US-0131449P.
 30-APR-1999; 99US-0132048P.
 04-MAY-1999; 99US-0132407P.
 05-MAY-1999; 99US-0132484P.
 06-MAY-1999; 99US-0132485P.
 06-MAY-1999; 99US-0132486P.
 07-MAY-1999; 99US-0132487P.
 11-MAY-1999; 99US-0132863P.
 14-MAY-1999; 99US-0134256P.
 14-MAY-1999; 99US-0134218P.
 14-MAY-1999; 99US-0134219P.
 14-MAY-1999; 99US-0134221P.
 14-MAY-1999; 99US-0134370P.
 18-MAY-1999; 99US-0134768P.
 19-MAY-1999; 99US-0134941P.
 20-MAY-1999; 99US-0135124P.
 21-MAY-1999; 99US-0135353P.
 24-MAY-1999; 99US-0135629P.
 25-MAY-1999; 99US-0136021P.
 27-MAY-1999; 99US-0136392P.
 28-MAY-1999; 99US-0136782P.
 01-JUN-1999; 99US-0137222P.
 03-JUN-1999; 99US-0137528P.
 04-JUN-1999; 99US-0137502P.
 07-JUN-1999; 99US-0137724P.
 08-JUN-1999; 99US-0138094P.
 10-JUN-1999; 99US-0138540P.
 10-JUN-1999; 99US-0138847P.
 14-JUN-1999; 99US-0139119P.
 16-JUN-1999; 99US-0139452P.
 16-JUN-1999; 99US-0139453P.
 17-JUN-1999; 99US-0139492P.
 18-JUN-1999; 99US-0139454P.
 18-JUN-1999; 99US-0139455P.
 18-JUN-1999; 99US-0139456P.
 18-JUN-1999; 99US-0139457P.
 18-JUN-1999; 99US-0139458P.
 18-JUN-1999; 99US-0139459P.
 18-JUN-1999; 99US-0139460P.
 18-JUN-1999; 99US-0139461P.
 18-JUN-1999; 99US-0139462P.
 18-JUN-1999; 99US-0139463P.
 18-JUN-1999; 99US-0139750P.
 18-JUN-1999; 99US-0139763P.
 21-JUN-1999; 99US-0139817P.
 22-JUN-1999; 99US-0139899P.
 23-JUN-1999; 99US-0140353P.
 23-JUN-1999; 99US-0140354P.
 24-JUN-1999; 99US-0140695P.
 28-JUN-1999; 99US-0140823P.
 29-JUN-1999; 99US-0140991P.
 30-JUN-1999; 99US-0141287P.
 01-JUL-1999; 99US-0141842P.
 01-JUL-1999; 99US-0142154P.
 02-JUL-1999; 99US-0142055P.
 06-JUL-1999; 99US-0142390P.
 08-JUL-1999; 99US-0142803P.
 09-JUL-1999; 99US-0142920P.
 12-JUL-1999; 99US-0142977P.
 13-JUL-1999; 99US-0143542P.
 14-JUL-1999; 99US-0143624P.
 15-JUL-1999; 99US-0144005P.
 16-JUL-1999; 99US-0144085P.
 16-JUL-1999; 99US-0144086P.
 19-JUL-1999; 99US-0144325P.
 19-JUL-1999; 99US-0144331P.

PF 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 23-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 18-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
PR 05-MAY-1999; 99US-0132484P.
PR 06-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132863P.
PR 14-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136382P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 21-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 15-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 26-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 03-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
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PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154032P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155565P.

QY 335 TEDNSTAVVVPFGWGKYKNSIN 358
 ID ABB07400 standard; protein; 423 AA.
 XX ABB07400;
 XX ABB07400;
 XX ABB07400;
 DT 09-APR-2002 (first entry)
 DE Amino acid sequence of protein seq Id No. 16 (Swiss Prot No. 004719).
 KW Protein phosphatase IIC ABI2; antiasthmatic; antiapoptotic; anti-HIV;
 KW neuroprotective; vasotrophic; virucide; osteopathic; cytostatic; human;
 KW antiinflammatory; anabolic; cancer.
 XX
 OS Homo sapiens.
 XX
 XX WO200196571-A2.
 FN
 XX
 PD 20-DEC-2001.
 XX
 XX 13-JUN-2001; 2001WO-EP006666.
 XX
 XX 16-JUN-2000; 2000US-0212043P.
 PR 07-AUG-2000; 2000US-0223322P.
 PR 13-DEC-2000; 2000US-0254877P.
 XX
 PA (FARB) BAYER AG.
 XX
 XX Xiao Y;
 PI
 XX
 XX WPI; 2002-139713/18.
 DR
 XX
 PT Protein phosphatase IIC ABI2 polypeptide and polynucleotides useful for
 PT identifying modulating agents useful in treating diseases e.g. cancer,
 PT inflammatory disorder, osteoporosis, asthma, AIDS and viral infections.
 XX
 PS Claim 37; Fig 16; 135pp; English.
 XX
 XX The invention relates to human protein phosphatase IIC ABI2 polypeptides
 CC and polynucleotides. The polypeptides can be expressed by standard
 CC recombinant methodology. The polypeptides, polynucleotides and modulators
 CC are useful for modulating activity of protein phosphatase IIC ABI2 in a
 CC disease or treating a disease which include asthma, chronic obstructive
 CC pulmonary disease (COPD), peripheral or central nervous system disease
 CC including neurodegenerative disease, a disorder associated with an
 CC increase in apoptosis, including AIDS and other infectious or genetic
 CC immunodeficiency, myelodysplasia, ischemic injury, toxin-induced disease,
 CC wasting disease, viral infection and osteoporosis, or disorder associated
 CC with decrease in apoptosis, including cancer and inflammatory disorder.
 CC Fusion proteins comprising protein phosphatase IIC ABI2 are useful for
 CC generating antibodies and for use in various assay systems, and the
 CC protein phosphatase IIC ABI2 polypeptide can also be used as a bait
 CC protein in a two-hybrid assay or three-hybrid assay. The present sequence
 CC represents the amino acid sequence of protein identified with Swiss Prot
 CC Accn No. 004719
 XX
 SQ Sequence 423 AA;
 Query Match 18.2%; Score 354.5; DB 5; Length 423;
 Best Local Similarity 30.6%; Pred. No. 1.2e-29;
 Matches 99; Conservative 51; Mismatches 99; Indels 75; Gaps 12;
 QY 96 GCASQIGKRNEDRFD-----FAQLTDEVL-----YFAYVDGGGPA 135
 DB 114 GVTICGRPEMEDSVSTIPFLQVSSSLDGRVTNGFNPHLSAHPFGYVDGGGQVA 173
 QY 136 DFCETHMEKICMDLLPKK-----NLETLTLAFLEIDKAFSSSHARLSADATLL 184

Db 174 NYCRRMHLALTEIIVKEKPEFCGDTWQEKWKALFNSFMRVDSIETVAHAPE----- 228
 QY 185 TSCTTATVALLRGGIELVVASVSDSRAILCRGKQMKLTIDHTPEKDKERIKKGG-P 243
 Db 229 TVGSTSVAVVFP-THIFVANGDSRAVLCKTKPLALSVDHKPDRDDAARIEAAGKV 287
 QY 244 VAWNSLQGFVNGRLAMTRSIGDLDLKTSGVIAEPE---TKRIKHADDLSFLVLTGDI 300
 Db 288 IRWNG--ARVFGVLAMSRISIGDYLKPS-VIPDEVTSVRRVK-----EDDCLILASDGL 339
 QY 301 NFMVNSQEIFCDFVQ-----CHDPN-----EAAHAYTEQAIQV 334
 Db 340 WDVMTNEEVCDLARKRILLWHKKNWAGEALLPAEKRGEGKDPAAASAAYLSKMAQKG 399
 QY 335 TEDNSTAVVVPFGWGKYKNSIN 358
 Db 400 SKDNISVVVVDLKGIRKFKSKSLN 423
 RESULT 34
 AAE04841
 ID AAE04841 standard; protein; 360 AA.
 XX
 AC AAE04841;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE Human SGP039 phosphatase polypeptide.
 XX
 KW Human; SGP039 phosphatase polypeptide; phosphatase-related disease;
 KW immune-related disorder; ocular disease; organ transplant rejection;
 KW infection; diabetes; pain; sexual dysfunction; Alzheimer's disease;
 KW metabolic disorder; haematopoietic cancer; mood disorder; cardiac;
 KW Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis;
 KW cardiovascular disease; brain; neuronal-associated disease; dyskinesia;
 KW attention disorder; cognition disorder; psychotic disorder; cytostatic;
 KW neurological disorder; virucide; nootropic; cerebrotective; therapy;
 KW neuroprotective; antibacterial; vulnery; tranquiliser; antiastrmatic;
 KW hypotensive; immunosuppressive; antipsoriatic; analgesic; hypertensive;
 KW antifungal; migraine; serine phosphatase; SGP; PP2C.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..301
 FT /label= Catalytic_domain
 FT Domain 91..344
 FT /label= Phosphatase_domain
 XX WO200146394-A2.
 PN
 PD 28-JUN-2001.
 XX
 XX 21-DEC-2000; 2000WO-US034736.
 XX
 XX 21-DEC-1999; 99US-0173255P.
 PR 28-DEC-1999; 99US-0175766P.
 PR 25-JAN-2000; 2000US-0178078P.
 PR 31-JAN-2000; 2000US-0179301P.
 XX
 XX (SUGB-) SUGEN INC.
 FA
 XX Plowman GD, Martinez R, Whyte D, Manning G, Sudarsanam S;
 PI Hill RJ, Flanagan P;
 XX WPI; 2001-418058/44.
 DR N-PSDB; AAD09493.
 XX Novel phosphatase polypeptide useful for treating cancers, immune-related
 PT diseases and disorders, cardiovascular disease, brain or neuronal-
 PT associated diseases and metabolic disorders.
 XX
 PS Claim 7; Fig 2; 186pp; English.

FT	Region	89. .349	/note= "Protein phosphatase 2C"
FT	Region	91. .344	/note= "Protein phosphatase 2C Pp2"
FT	Region	97. .360	/note= "Protein phosphatase 2C"
FT	Region	97. .276	/note= "Protein phosphatase 2C magnesium hydrolase manganese multigene family PP2C isoform"
FT	Region	99. .109	/note= "Protein phosphatase 2C p"
FT	Region	123. .132	/note= "Protein phosphatase 2C p"
FT	Region	123. .131	/note= "Protein phosphatase 2C Pp2c"
FT	Region	210. .249	/note= "Protein phosphatase 2C p"
FT	Region	256. .269	/note= "Protein phosphatase 2C p"
FT	Region	294. .306	/note= "Protein phosphatase 2C p"
FT	Region	340. .349	/note= "Protein phosphatase 2C p"
XX	WO200210363-A2.		
PN	07-FEB-2002.		
XX	26-JUL-2001; 2001WO-US023716.		
XX	28-JUL-2000; 2000US-0221679P.		
PR	03-AUG-2000; 2000US-0223272P.		
PR	10-AUG-2000; 2000US-0224309P.		
PR	18-AUG-2000; 2000US-0226728P.		
PR	30-AUG-2000; 2000US-0229254P.		
PR	08-SEP-2000; 2000US-0231366P.		
XX	(INCY-) INCYTE GENOMICS INC.		
XX	Tang YT, Elliott VS, Ramkumar J, Yao MG, Burford N, Wang YE; Stewart EA, Gandhi AR, Paterson C, Lee EA, Hafalia AJA, Lu DAM; Tribouley CM, Griffin JA, Baughn MR, Yue H, Warren BA, Nguyen DB; Walla NK, Kearney L;		
XX	MP1; 2002-188735/24.		
DR	N-PSDB; ABK14469.		
XX	New protein phosphatases, useful for diagnosing, treating or preventing immune system disorders (e.g. Crohn's disease), neurological disorders (e.g. Parkinson's disease), or cell proliferative disorders (e.g. cancers).		
PT	Claim 1; Page 102; 117pp; English.		
XX	The present invention relates to a new polypeptide, a naturally occurring amino acid sequence at least 95 % identical to it, a biologically active fragment of it or an immunogenic fragment of it. The polypeptides, polynucleotides, agonists and antagonists are useful for diagnosing, treating or preventing disorders associated with aberrant expression of protein phosphatases (PP), particularly immune system disorders e.g. acquired immunodeficiency syndrome (AIDS), thymic hypoplasia, anaemia, asthma or Crohn's disease, neurological disorders e.g. epilepsy, Huntington's disease, dementia or Parkinson's disease, developmental disorders e.g. Down's syndrome, or cell proliferative disorders e.g. cancers including adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma or sarcoma. The present amino acid sequence represents human protein phosphatase 2 (Pp2) which is one of several human protein phosphatases (AAU75783-AAU75792) of the invention		
XX	Sequence 360 AA;		
XX	Query Watch	18.0%;	Score 350.5; DB 5; Length 360;
XX	Best Local Similarity	34.3%;	Pred. No. 2.5e-29;

Matches	95;	Conservative	52;	Mismatches	101;	Indels	29;	Gaps	11;
QY	94	NVGCASQIGRKENEDRF----	DFAQUTDEVLYPAVYDGHGGPAAADFCHTHMEKCI	MDL	149				
Db	92	NVAVYSIQRRDHMEDRFVLTLDLANKTHPSI-FGIFDGHGGETAEEVVKSRUPEAL	KQH	150					
QY	150	L---PKEK-----NLETLITLAFLEIDKAPSSSHARLSADATLLTSGTTATVALLR	GIEL	201					
Db	151	LQYVEKDKENSUSYQITLQQQLISIDREMLEKLTVSYD----	EAGTTCIALLSDK-DL	205					
QY	202	VWASVGDSSRAILCRK-GKPMKLTITDHTPERKDEKERIKKCGGFVAMNSLGQPHVNGSLAM	260						
Db	206	TVANVGDSSRGVLCDDKGNAPLSHSHDKPYQLKEKR	IKRAGGFISFN--GSRVQVQIGILAM	263					
QY	261	TRSGDLDLKT-SGVIAEPETKRILHHADDSFLVLTDTG	INFMVNSQEICDFVNO-CHD	318					
Db	264	SRLSGDYPLKRLNVVIPPDLITFDLDKLOPEPFMILASDGLMDAFSNEEA	VRFTIKERLDE	323					
QY	319	PNEAAHVAVTQAIQYGTEDNSTAVVPFGAWGKYKNS	355						
Db	324	PHFGAKSIVLQSFYRGCPDNI	TWVV-----KPRNS	354					
RESULT	36								
ABB78060	ID	ABB78060	standard; protein; 274 AA.						
XX	AC	ABB78060;							
XX	AC	ABB78060;							
DT	05-NOV-2002	(first entry)							
XX	Consensus	sequence derived from a hidden Markov model from PFAM.							
DE	Human; 16105;	cancer; cellular proliferation disorder; brain cancer;							
KW	cellular	differentiation disorder; breast cancer; lung cancer;							
KW	ovarian	cancer; cardiovascular disorder; hypertension; atherosclerosis;							
KW	arrhythmia;	heart failure; endothelial cell disorder; psoriasis;							
KW	Grave's	disease; autoimmune disease; diabetes mellitus; Crohn's disease;							
XX	viral	disease; pain; metabolic disorder.							
OS	Synthetic.								
PN	US2002077463-A1.								
PD	20-JUN-2002.								
PF	17-MAY-2001; 2001US-00860351.								
XX	19-MAY-2000; 2000US-0205260P.								
PR	(MEYE/) MEYERS R.								
PA	Meyers R;								
PI	WPI; 2002-607448/65.								
DR	New polypeptide for treating a subject having a disorder or at risk of								
PT	developing a proliferative disorder, cardiovascular disorder, autoimmune								
PT	or metabolic disorder.								
XX	Disclosure; Fig 3; 50pp; English.								
PS									
XX									
CC	The specification describes a human polypeptide, designated 16105. 16105								
CC	polypeptides and polynucleotides are used for evaluating the efficacy of								
CC	a treatment of cancer or a cellular proliferation and/or differentiation								
CC	disorder in a subject. They are also useful for diagnosing a cancer or a								
CC	cellular proliferation and/or differentiation disorder in a subject. The								
CC	cancer or cellular proliferation and/or differentiation is breast, lung,								
CC	brain or ovarian cancer. They may also be used for treating proliferative,								
CC	disorders e.g., cancer; cardiovascular disorders e.g., hypertension,								
CC	atherosclerosis, arrhythmias, heart failure; endothelial cell disorders								
CC	e.g., psoriasis, Grave's disease; autoimmune diseases e.g., diabetes								
CC	mellitus, Crohn's disease; viral diseases; pain; or metabolic disorders.								

XX Claim 37; Fig 14; 135pp; English.
 XX
 CC The invention relates to human protein phosphatase IIC ABI2 polypeptides
 CC and polynucleotides. The polypeptides can be expressed by standard
 CC recombinant methodology. The polypeptides, polynucleotides and modulators
 CC are useful for modulating activity of protein phosphatase IIC ABI2 in a
 CC disease or treating a disease which include asthma, chronic obstructive
 CC pulmonary disease (COPD), peripheral or central nervous system disease
 CC including neurodegenerative disease, a disorder associated with an
 CC increase in apoptosis, including AIDS and other infectious or genetic
 CC immunodeficiency, myelodysplasia, ischemic injury, toxin-induced disease,
 CC wasting disease, viral infection and osteoporosis; or disorder associated
 CC with decrease in apoptosis, including cancer and inflammatory disorder.
 CC Fusion proteins comprising protein phosphatase IIC ABI2 are useful for
 CC generating antibodies and for use in various assay systems, and the
 CC protein phosphatase IIC ABI2 polypeptide can also be used as a bait
 CC protein in a two-hybrid assay or three-hybrid assay. The present sequence
 CC represents a human protein phosphatase IIC ABI2 polypeptide
 XX
 SQ Sequence 76 AA;
 Query Match 17.8%; Score 348; DB 5; Length 76;
 Best Local Similarity 98.5%; Pred. No. 3.7e-30;
 Matches 66; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 234 KERIKCGGFVANNLSGQPHVNGRLAMTRISIGDLTKTSGVIAEPETKRIKLHADDGSL 293
 DB 1 KERIKCGGFVANNLSGQPHVNGRLAMTRISIGDLTKTSGVIAEPETKRIKLHADDGSL 60
 QY 294 VLTTDGI 300
 DB 61 VLTTDGL 67
 RESULT 38
 AAE01349
 ID AAE01349 standard; protein; 423 AA.
 AC AAE01349;
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Arabidopsis thaliana ABA (abscisic acid)-insensitive 2, abi2 mutant.
 XX
 KW Abscisic acid; ABA; ABA-insensitive, abi2; signal transduction;
 KW kernel embryo promoter; cereal plant; maize; rice; cotton; citrus tree;
 KW tomato; pine; soybean; peanut; olive; mutant; mutein.
 XX
 OS Arabidopsis thaliana.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 168
 FT /note= "Wild type Gly substituted with Asp"
 XX
 PN W0200136596-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 17-NOV-2000; 2000WO-US031739.
 XX
 PR 17-NOV-1999; 99US-0166080P.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Helentjaris T;
 XX
 DR WPI; 2001-329218/34.
 DR N-PSDB; AAD05668.
 XX
 PT DNA constructs containing an abscisic acid-associated sequence are used
 PT to modulate a response in a plant to abscisic acid so that the plants are
 PT protected against any harmful or detrimental effects of stress and

XX environmental conditions.
 PS Claim 5; Page; 60pp; English.
 XX
 CC The invention relates to a method for modulating a response in a target
 CC plant to abscisic acid (ABA) by introducing a DNA construct comprising an
 CC ABA-associated sequence operably linked to an early kernel/embryo
 CC promoter into the plant. The method also involves modulating ABA
 CC perception and signal transduction in developing seeds. The method is
 CC used to produce plants, particularly cereal plants such as maize, which
 CC have a modified response to ABA so that an increase in yield can be
 CC produced. The plants are protected against any harmful/detrimental
 CC effects of stress and adverse environmental conditions. The ABA function
 CC is disrupted in a tissue and developmental preferred manner so that
 CC female reproductive tissue is insulated from the stress or adverse
 CC environmental conditions. Other plants which can be transformed include
 CC rice, cotton, citrus trees, tomatoes, pines, soybean, peanut and olive.
 CC The present sequence is Arabidopsis thaliana ABA-insensitive 2 (abi2) but
 CC mutant. Note: The present sequence is not shown in the specification but
 CC is derived from ABI2 protein referred as SED ID NO: 6 (AAE01345) and
 CC shown in sequence listing of the specification
 XX
 SQ Sequence 423 AA;
 Query Match 17.8%; Score 347.5; DB 4; Length 423;
 Best Local Similarity 30.2%; Pred. No. 6.9e-29;
 Matches 98; Conservative 51; Mismatches 100; Indels 75; Gaps 12;
 QY 96 GCASQICKRKENEDRPD---FAQLTDEVL-----VFAYVDGHGGPAAA 135
 DB 114 GVTISICGRPEMEDSVSTIPRFLOVSSSSLLDGRVTNGFNPHLSAHFFGVYDGHDSQVA 173
 QY 136 DFCETHMEKICIMDLLPKEK-----NLETLLTFLAFLEITDKAFSSHARLSADATLL 184
 DB 174 NYCRRMHLALTEIVEKEPEFCDGTWQEKWKALKFNSFMRYDSEITVAHAPE----- 228
 QY 185 TSGTTATVALLRDGIELVVASVGSRAILCRKPKMKLTIDHTPERKDEKRIKCGG-F 243
 DB 229 TVGSTVAVVFP-THIFVANGDSRAVLCRGKTPALSVDHPRDDDEARIEAGGKV 287
 QY 244 VANNLSGQPHVNGRLAMTRISIGDLTKTSGVIAEPE---TKRIKLHADDGSLVLTDDGI 300
 DB 288 IRWNG---AAVFGVLAWSRISIGDRLKPS-VIPDEPVTSVRVK---EDDCILASDGL 339
 QY 301 NFMVNSOEICDFVNO---CHDFN-----EAAHAVTEQAIQVG 334
 DB 340 WDVMTNEVCDLARKRILLWHKKNAMAGEALLPAEKKGEGKDPAAWSAAEYLSKMALQKG 399
 QY 335 TEDNSTAVVVPFGAWGKYKNSIN 358
 DB 400 SKDNISVVVDLKGIRKFKSKSLN 423
 RESULT 39
 AAG06998
 ID AAG06998 standard; protein; 309 AA.
 AC AAG06998;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 3981.
 XX
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX
 OS Arabidopsis thaliana.
 XX
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.
 XX

PF 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 23-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 08-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134258P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 19-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137223P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
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PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
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PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
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Query Match 17.5%; Score 342; DB 3; Length 393;
Best Local Similarity 31.0%; Pred. No. 2.4e-28;
Matches 103; Conservative 50; Mismatches 127; Indels 52; Gaps 10;
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DB 22 SAKXWD-----TAGEKRLSLVDMPEKVDGCGYGGWKN-----DDGSL- 63
QY 78 PPSIKYGPFPKISLENVCASQIGKXKENEEDRFDAQLTDE---VLYPAYVDHGHPAA 134
DB 64 -----SCGYCSFRGKRSTMEDFYDIKASTIEGQAVCMFGIFDGHGSGRA 107
QY 135 ADFCHTHMEKIMDLLPKENKLETLTLTFLAFLDKAFSHARLSADATLLTSGTTATVAL 194
DB 108 ABLKHELFNNLMKHPQFILTDLKALNETYKQTDVAFLE-----SEKDYRDDGSTASAAV 163
QY 195 LRDGIELVWASGDSRAILCRKPKMKLTIDHTPERKDEKRIKKGCGFVANSIGQPHV 254

DB 164 L-VGNHLYVANVGDSRTIVSKAGKAIASDDHKPNRSDEKRIESAGGVIMW--AGTWRV 220
QY 255 NGRLAMTRISGDLDIKTSGVTAEPETKRIKLHADDSDLVLTDTGDNFMVNSQICDFVN 314
DB 221 GGVILAMSAFGNMLK-QFVVAEPEIQDLEIDH-EALLVLASDGLWDVVNEBAVALAQ 278
QY 315 QCHDPNEAAHAHVTEQAIQYGTEDNSTAVVVPF 346
DB 279 SEEPERAAARKLTDATFRSGSADNITCIVKVF 310
RESULT 42
AAG39774
ID AAG39774 standard; protein; 420 AA.
XX AAG39774;
AC AAG39774;
DT 18-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 49264.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 49264.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
XX EP1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
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Query Match 17.5%; Score 342; DB 3; Length 420;
Best Local Similarity 31.0%; Pred. No. 2.8e-28;

Matches 103; Conservative 50; Mismatches 127; Indels 52; Gaps 10;

QY

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Qy	78	PPSIKYGKPIKISLENVGCASQIGKEKENEEDRFDFAQLTDE---VLYFAVYDGHGSPAA	134	PR	19-MAY-1999;	99US-0134941P.
Db	101	-----SCGYCSPRGKSTMEDFYDIKASTIEGQAVCMFGIEDGHGGSRA	144	PR	20-MAY-1999;	99US-0135124P.
Qy	135	ADPCHTMEKIMDILLPEKKNLETLTLTFLAFLDIDKAFSSHARLSADATILTSGTATVAL	194	PR	21-MAY-1999;	99US-0135353P.
Db	145	AEYLKEHLFNNLMKHPOFLDTKLALNETYKQTDVAFLE-----SEKDYRDDGSGTASAAV	200	PR	24-MAY-1999;	99US-0135629P.
Qy	195	LRDGIELVAVSGVDSRAILCRKKGPKMLTIDHTPERKDEKERIKKCGGFVAVNSLGGPHV	254	PR	25-MAY-1999;	99US-0136021P.
Db	201	L-VGNHLYVANVGSRTIVSKAGRAIALSDHKENRSDERKRIESAGGVIMW--AGTRV	257	PR	27-MAY-1999;	99US-0136392P.
Qy	255	NGLIANTRSIGDLIKTSQVTAEPETKRIKLHHADDSFLVLTDDGINFPMVNSQEBICDFVN	314	PR	28-MAY-1999;	99US-0136782P.
Db	258	GGVLAMSAFNGRMVK-QFVVAEPIQOLEIDH-EAELLVLASDGLWDVVPNEADAVALQ	315	PR	01-JUN-1999;	99US-0137222P.
Qy	315	QCHDPNEAAHVAVTQALQYGTEDNSTAVVVPF	346	PR	03-JUN-1999;	99US-0137528P.
Db	316	SEEPPEAAARKLTDATSRGSDADNITCIVVKF	347	PR	04-JUN-1999;	99US-0137502P.
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XX						99US-0139452P.
AC	AAG39776;					99US-0139453P.
DT	18-OCT-2000 (first entry)					99US-0139454P.
XX						99US-0139455P.
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 49266.					99US-0139456P.
XX						99US-0139457P.
KW	Protein identification; signal transduction pathway; metabolic pathway;					99US-0139458P.
KW	hybridisation assay; genetic mapping; gene expression control; promoter;					99US-0139460P.
XX	termination sequence.					99US-0139461P.
XX						99US-0139462P.
OS	Arabidopsis thaliana.					99US-0139463P.
XX						99US-0139464P.
PN	EP1033405-A2.					99US-0139465P.
PD	06-SEP-2000.					99US-0139466P.
XX						99US-0139467P.
PF	25-FEB-2000; 2000EP-00301439.					99US-0139468P.
XX						99US-0139469P.
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PR	25-MAR-1999; 99US-0126264P.					99US-0139474P.
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PR	21-APR-1999; 99US-0130449P.					99US-0139481P.
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PR	28-APR-1999; 99US-0130891P.					99US-0139483P.
PR	30-APR-1999; 99US-0131449P.					99US-0139484P.
PR	04-MAY-1999; 99US-0132048P.					99US-0139485P.
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PR 18-OCT-1999; 99US-0159584P.
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Query Match 17.5%; Score 341.5; DB 3; Length 358;
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QY	94	NVGCASQIGKKRKENEDRPDPQAULTDE---VLIFYAVDGHGGPAAADPFCHTHMKCIMDLL 150
DB	39	SCGYCSFRGKRSTMEDFYDIKASTIEQACVMCFIDHGGGSRAAEYLKEHLFNLMKHP 98
QY	151	PKEKNLETLTLLAFLEIDKRAFSSHARLSADATLITSGTTATVALLDGTELVVASVGDSR 210
DB	99	QFLTDTKLALNETYKTODVAFL-----SEKDTVRDDGSTASAVAL-VGNHLYVANVGDSR 153
QY	211	AILCRXGKPMKLAIDHTPERKDSEIRIKKCGGFVAWNLSQPQHVNGLAMTRSIGDLDLK 270
DB	154	TIVSKAGKALASDDHKPNESDERKRIESAGGVIMW--AGTWREVGGVLMSRAFGNMLK 211
QY	271	TSGVIAPETKRIKLHHADDPSFVLTTDGINFMVNSQEICDFVNOCHDPNEAAHAATEQA 330
DB	212	-QFWAEPETQDLEIDH-EAELLIVLASDGLWVPVEDAVAALACSBEPEAAAARKLTDTA 269
QY	331	IQTGTEDNSTAVVVVF 346
DB	270	FRRGSADNITCIUVKF 285

RESULT 45
 AAG18040 ID ID AAG18040 standard; protein; 359 AA.
 XX AC AAG18040;
 XX DT 17-OCT-2000 (first entry)
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 19291.
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX Arabidopsis thaliana.
 OS EP1033405-A2.
 XX PN 06-SEP-2000.
 PD 25-FEB-2000; 2000EP-00301439.
 PF 25-FEB-1999; 99US-0121825P.
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KW Protein identification; signal transduction pathway; metabolic pathway;
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XX 17-OCT-2000 (first entry)

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XX Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

XX Arabidopsis thaliana.

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PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
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PR 14-OCT-1999; 99US-0159329P.
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PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
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PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
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PR 28-OCT-1999; 99US-0161993P.
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Query Match 17.4%; Score 338.5; DB 3; Length 360;
Best Local Similarity 30.9%; Pred. No. 5.3e-28;
Matches 99; Conservative 60; Mismatches 132; Indels 29; Gaps 11;
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QY 94 NVGCASQIGKXKXENEDPFAQLTD----EVLVAYVDHGGAADFCHTHMEKIM-- 147
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Db 171 DDFISDTKK-----AIVFVQOTDEBYLIERAGQPKNAGSTAATALL-IGDKLIVANV 222
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Db 223 GDSVAVSRNGSAVPLSDHDKPDSRDERQIEDAGGFLIW--AGTWKVGILAVSRAFGD 280
Qy 267 LDLTSGTVIAPETPKRIKLHADDSTFLVLTDTGINFVMSQEQICDFVNOCHDNEAAHAV 326
Db 281 KQLKPY-VIAPETQEBDISTLE--FIVASDGLWNLNKDAVAIVRDISDAETAAIKL 337
Qy 327 TEQAIQYQGTEDNSTAVVVPF 346
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ID AAE01344 standard; protein; 434 AA.
AC AAE01344;
XX
DT 31-JUL-2001 (first entry)
DE Arabidopsis thaliana ABA (abscisic acid)-insensitive 1, ABI1 protein.
KW Abscisic acid; ABA; ABA-insensitive; ABI1; signal transduction;
KW kernel embryo promoter; cereal plant; maize; rice; cotton; citrus tree;
KW tomato; pine; soybean; peanut; olive.
XX
OS Arabidopsis thaliana.
XX
PN WO200136596-A2.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-US031739.
XX
PR 17-NOV-1999; 99US-0166080P.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Helentjaris T;
XX
WPI; 2001-329218/34.
DR N-PSDB; AAD05660.
XX
XX DNA constructs containing an abscisic acid-associated sequence are used
PT to modulate a response in a plant to abscisic acid so that the plants are
PT protected against any harmful or detrimental effects of stress and
PT environmental conditions.
XX
PS Claim 3; Page 46; 60pp; English.
XX
XX The invention relates to a method for modulating a response in a target
CC plant to abscisic acid (ABA) by introducing a DNA construct comprising an
CC ABA-associated sequence operably linked to an early kernel/embryo
CC promoter into the plant. The method also involves modulating ABA
CC perception and signal transduction in developing seeds. The method is
CC used to produce plants, particularly cereal plants such as maize, which
CC have a modified response to ABA so that an increase in yield can be
CC produced. The plants are protected against any harmful/detrimental
CC effects of stress and adverse environmental conditions. The ABA function
CC is disrupted in a tissue and developmental preferred manner so that
CC female reproductive tissue is insulated from the stress or adverse
CC environmental conditions. Other plants which can be transformed include
CC rice, cotton, citrus trees, tomatoes, pines, soybean, peanut and olive.
CC The present sequence is Arabidopsis thaliana ABA-insensitive 1 (ABI1)
CC protein
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SQ Sequence 434 AA;
Query Match 17.3%; Score 338; DB 4; Length 434;

Best Local Similarity 30.9%; Pred. No. 8.1e-28;
Matches 100; Conservative 46; Mismatches 98; Indels 80; Gaps 12;
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Db 351 DVMTDEEACEAMARKILLWHKKNVAGDASILLADERRRKEGKDPAAAMSAAYLSKLAIO 410
Qy 335 TEDNSTAVVVPFGANGKYNSEIN 358
Db 411 SKDNISVVVVVDLKPRLKSKPLN 434
RESULT 49
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ID AAE36344 standard; protein; 434 AA.
XX
AC AAE36344;
XX
DT 26-JUN-2003 (first entry)
DE Arabidopsis thaliana LMP encoded by pk105 cDNA clone.
XX
KW Lipid metabolism protein; LMP; seed storage; transgenic; plant; cress.
XX Arabidopsis thaliana.
XX
PN WO200299076-A2.
XX
PD 12-DEC-2002.
XX
PF 04-JUN-2002; 2002WO-US017937.
XX
PR 04-JUN-2001; 2001US-0295680P.
XX
PA (BADI) BASP PLANT SCI GMBH.
XX
PI Mittendorf V, Haertel H, Cirpus P;
XX
WPI; 2003-140611/13.
DR N-PSDB; AAD54922.
XX
XX New isolated lipid metabolism protein (LMP) nucleic acids and proteins
PT modulating seed storage compound in a plant, useful for producing
PT transgenic plants with modified or increased lipids, fatty acids,
PT cofactors and enzymes.
XX
PS Claim 2; Fig 22B; 52pp; English.
XX
XX The invention relates to lipid metabolism protein (LMP) nucleic acids and
CC proteins modulating seed storage compound in a plant. The invention also
CC relates to a method for producing a transgenic plant having a modified
CC level of a seed storage compound, which involves transforming a plant
CC cell with an expression vector having LMP. The method is useful for
CC modifying or increasing lipids and fatty acids, cofactors and enzymes in
CC transgenic plants. The present sequence is Arabidopsis thaliana LMP
CC protein
XX

SQ Sequence 434 AA;
 Query Match 17.3%; Score 338; DB 6; Length 434;
 Best Local Similarity 30.9%; Pred. No. 8.1e-28;
 Matches 100; Conservative 46; Mismatches 98; Indels 80; Gaps 12;

QY 96 GCASQIGKRNED-----RFDPAQLTDEVLYFVYDGHGGPAAAD 136
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 DB 411 SKNISVVVVLDKPRKLSKPLN 434

RESULT 50
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 ID AAE01348 standard; protein; 434 AA.
 XX AAE01348;
 AC AAE01348;
 XX 31-JUL-2001 (first entry)
 XX Arabidopsis thaliana ABA (abscisic acid)-insensitive 1, abil mutant.
 DE Arabidopsis thaliana ABA (abscisic acid)-insensitive 1, abil mutant.
 XX Abscisic acid; ABA; ABA-insensitive, abil; signal transduction;
 KW kernel embryo promoter; cereal plant; maize; rice; cotton; citrus tree;
 KW tomato; pine; soybean; peanut; olive; mutant; mutein.
 XX Arabidopsis thaliana.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 180
 FT /notes= "Wild type Gly substituted with Asp"
 XX
 XX WO200136596-A2.
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 XX 25-MAY-2001.
 XX
 XX 17-NOV-2000; 2000WO-US031739.
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 XX 17-NOV-1999; 99US-0166080P.
 XX
 XX (PION-) PIONEER HI-BRED INT INC.
 XX
 XX Helentjaris T;
 XX
 XX WPI; 2001-329218/34.
 DR N-PSDB; AAD05667.
 XX
 XX DNA constructs containing an abscisic acid-associated sequence are used
 PT to modulate a response in a plant to abscisic acid so that the plants are
 PT protected against any harmful or detrimental effects of stress and
 PT environmental conditions.
 XX
 XX Claim 5; Page; 60pp; English.

CC The invention relates to a method for modulating a response in a target
 CC plant to abscisic acid (ABA) by introducing a DNA construct comprising an
 CC ABA-associated sequence operably linked to an early kernel/embryo
 CC promoter into the plant. The method also involves modulating ABA
 CC perception and signal transduction in developing seeds. The method is
 CC used to produce plants, particularly cereal plants such as maize, which
 CC have a modified response to ABA so that an increase in yield can be
 CC produced. The plants are protected against any harmful/detrimental
 CC effects of stress and adverse environmental conditions. The ABA function
 CC is disrupted in a tissue and developmental preferred manner so that
 CC female reproductive tissue is insulated from the stress or adverse
 CC environmental conditions. Other plants which can be transformed include
 CC rice, cotton, citrus trees, tomatoes, pines, soybean, peanut and olive.
 CC The present sequence is a Arabidopsis thaliana ABA-insensitive 1 (abil)
 CC mutant. Note: The present sequence is not shown in the specification but
 CC is derived from AB11 protein referred as SED ID NO: 4 (AAE01344) and
 CC shown in sequence listing of the specification

XX SQ Sequence 434 AA;

Query Match 17.0%; Score 331; DB 4; Length 434;
 Best Local Similarity 30.6%; Pred. No. 4.8e-27;
 Matches 99; Conservative 46; Mismatches 99; Indels 80; Gaps 12;

QY 96 GCASQIGKRNED-----RFDPAQLTDEVLYFVYDGHGGPAAAD 136
 DB 130 GFTSICGRPEMEDAVSTIPRFLOSSSGSMLDGRFPQSAAH---PFGVYDGHGGSQVAN 186
 QY 137 FCHTHMEKCMIDLPLPEKNL-----ETLLTLAFLFLEIDKAFSSSHARLSADATLLT 185
 DB 187 YCEREMHLALAEIAKEKPMLCDGDTWLEKWKALFNSFLRVDSEIESVAP-----ET 239
 QY 186 SGTATVALLRDGIELVVASVGSRAILCRKPKMLTIDHTPERKDEKERIKKCGG-FV 244
 DB 240 VGSTSVAVVFPF-HIFVANCGRSRAVLCRGKTALPLSDHFKPDEDEAARIEAAGKVI 298
 QY 245 Awnslgophvngriamtrstgldlktsgviaepe---TKRIKLHADDsFLVLTDDGIN 301
 DB 299 QWNG---ARVFGVLAMRSRSGDRLKPS-IIPPEVTAVKRVK-----EDDCILASDGWV 350
 QY 302 FMVNSQICDFVQ---CHDPN-----EAAHVAVTEQAIQVG 334
 DB 351 DVMTDEACEWARKRILLWHKKNVAGDASLLADERKKGKOPAAVSAAYLSKLAIQRG 410
 QY 335 TEDNSTAVVVPFGAWGKYKNSIN 358
 DB 411 SKNISVVVVLDKPRKLSKPLN 434

Search completed: October 17, 2004, 15:25:37
 Job time : 101 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 17, 2004, 15:21:58 ; Search time 93 Seconds
(without alignments)

1287.197 Million cell updates/sec

Title: US-10-716-488-2

Perfect score: 1951
Sequence: 1 MSTAALTLVRSGNQVRR.....KNSINFSPRSPASSGRWA 372

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 75 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1951	100.0	372	9	US-09-973-084-4
3	1951	100.0	372	9	US-09-973-077-4
4	1951	100.0	372	9	US-09-973-063-4
5	1951	100.0	372	9	US-09-973-964-4
6	1951	100.0	372	9	US-09-975-072-4
7	1951	100.0	372	9	US-09-972-038-4
8	1951	100.0	372	9	US-09-972-757-4
9	1951	100.0	372	9	US-09-973-965-4
10	1951	100.0	372	9	US-09-973-941-4
11	1951	100.0	372	10	US-09-986-992-2
12	1951	100.0	372	10	US-09-971-782-4
13	1951	100.0	372	16	US-10-311-764-1
14	1951	100.0	372	16	US-10-716-488-2
15	1951	100.0	372	15	US-10-716-489-2

ALIGNMENTS

RESULT 1
US-09-973-963-4
; Sequence 4, Application US/09973963
; Patent No. US20020106676A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen

Sequence 1699, Ap
Sequence 2487, Ap
Sequence 1655, Ap
Sequence 2, Appli
Sequence 44, Appl
Sequence 3238, Ap
Sequence 853, App
Sequence 854, App
Sequence 4, Appli
Sequence 35, Appl
Sequence 164347,
Sequence 219801,
Sequence 176581,
Sequence 66152, A
Sequence 65340, A
Sequence 62620, A
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RESULT 4
US-09-973-063-4
; Sequence 4, Application US/09973063
; Patent No. US20020115119A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,063
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-063-4

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; Sequence 4, Application US/09973964
; Patent No. US20020115606A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,964
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 60/304,775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-964-4

Query Match 100.0%; Score 1951; DB 9; Length 372;
Best Local Similarity 100.0%; Pred. No. 4.3e-205; Indels 0; Gaps 0;
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; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/975,072
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-975-072-4

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Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSTAALITLVRSNGQVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRFPDGGSPAT 60
QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIKISLENVGCASQIGKRKENEFRDFAQLTDEV 120
DB 61 WDNFGIWDNRIDEPILLPPSIKYGKPIKISLENVGCASQIGKRKENEFRDFAQLTDEV 120
QY 121 LYFAVYDGHGGAADFCCHTHMEKICMDLLPKENLETLTLAFLAIDKAFSSHARLSAD 180
DB 121 LYFAVYDGHGGAADFCCHTHMEKICMDLLPKENLETLTLAFLAIDKAFSSHARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPMKLTIDHTPERKDEKERIKK 240
DB 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPMKLTIDHTPERKDEKERIKK 240
QY 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLKTSVIAEPETKRIKLHHADDSFLVLTDDGI 300
DB 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLKTSVIAEPETKRIKLHHADDSFLVLTDDGI 300
QY 301 NFMVNSOEICDFVNOCHDPNEAAHVAHQIAOYGTEDNSTAVVVPFGAWGKYKNSINFS 360
DB 301 NFMVNSOEICDFVNOCHDPNEAAHVAHQIAOYGTEDNSTAVVVPFGAWGKYKNSINFS 360
QY 361 FSRSFASSGRWA 372
DB 361 FSRSFASSGRWA 372

RESULT 7
US-09-972-038-4
; Sequence 4, Application US/09972038
; Patent No. US20020119155A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/972,038
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-038-4

Query Match
Best Local Similarity 100.0%; Score 1951; DB 9; Length 372;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSNGQVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRFPDGGSPAT 60
DB 1 MSTAALITLVRSNGQVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRFPDGGSPAT 60
QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIKISLENVGCASQIGKRKENEFRDFAQLTDEV 120
DB 61 WDNFGIWDNRIDEPILLPPSIKYGKPIKISLENVGCASQIGKRKENEFRDFAQLTDEV 120
QY 121 LYFAVYDGHGGAADFCCHTHMEKICMDLLPKENLETLTLAFLAIDKAFSSHARLSAD 180
DB 121 LYFAVYDGHGGAADFCCHTHMEKICMDLLPKENLETLTLAFLAIDKAFSSHARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPMKLTIDHTPERKDEKERIKK 240
DB 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPMKLTIDHTPERKDEKERIKK 240
QY 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLKTSVIAEPETKRIKLHHADDSFLVLTDDGI 300
DB 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLKTSVIAEPETKRIKLHHADDSFLVLTDDGI 300
QY 301 NFMVNSOEICDFVNOCHDPNEAAHVAHQIAOYGTEDNSTAVVVPFGAWGKYKNSINFS 360
DB 301 NFMVNSOEICDFVNOCHDPNEAAHVAHQIAOYGTEDNSTAVVVPFGAWGKYKNSINFS 360
QY 361 FSRSFASSGRWA 372
DB 361 FSRSFASSGRWA 372

RESULT 7
US-09-972-038-4
; Sequence 4, Application US/09972038
; Patent No. US20020119155A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/972,038
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-038-4

Query Match
Best Local Similarity 100.0%; Score 1951; DB 9; Length 372;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSNGQVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRFPDGGSPAT 60
DB 1 MSTAALITLVRSNGQVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRFPDGGSPAT 60
QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIKISLENVGCASQIGKRKENEFRDFAQLTDEV 120
DB 61 WDNFGIWDNRIDEPILLPPSIKYGKPIKISLENVGCASQIGKRKENEFRDFAQLTDEV 120
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DB 61 WDNFGIWDNRIDEPILLPPSIKYGKPIKISLENVGCASQIGKRKENEFRDFAQLTDEV 120
QY 121 LYFAVYDGHGGAADFCCHTHMEKICMDLLPKENLETLTLAFLAIDKAFSSHARLSAD 180
DB 121 LYFAVYDGHGGAADFCCHTHMEKICMDLLPKENLETLTLAFLAIDKAFSSHARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPMKLTIDHTPERKDEKERIKK 240
DB 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPMKLTIDHTPERKDEKERIKK 240
QY 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLKTSVIAEPETKRIKLHHADDSFLVLTDDGI 300
DB 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLKTSVIAEPETKRIKLHHADDSFLVLTDDGI 300
QY 301 NFMVNSOEICDFVNOCHDPNEAAHVAHQIAOYGTEDNSTAVVVPFGAWGKYKNSINFS 360
DB 301 NFMVNSOEICDFVNOCHDPNEAAHVAHQIAOYGTEDNSTAVVVPFGAWGKYKNSINFS 360
QY 361 FSRSFASSGRWA 372
DB 361 FSRSFASSGRWA 372

RESULT 8
US-09-972-757-4
; Sequence 4, Application US/09972757
; Patent No. US20020119927A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/972,757
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-757-4

Query Match
Best Local Similarity 100.0%; Score 1951; DB 9; Length 372;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSNGQVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRFPDGGSPAT 60
DB 1 MSTAALITLVRSNGQVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRFPDGGSPAT 60
QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIKISLENVGCASQIGKRKENEFRDFAQLTDEV 120
DB 61 WDNFGIWDNRIDEPILLPPSIKYGKPIKISLENVGCASQIGKRKENEFRDFAQLTDEV 120
QY 121 LYFAVYDGHGGAADFCCHTHMEKICMDLLPKENLETLTLAFLAIDKAFSSHARLSAD 180
DB 121 LYFAVYDGHGGAADFCCHTHMEKICMDLLPKENLETLTLAFLAIDKAFSSHARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPMKLTIDHTPERKDEKERIKK 240
DB 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPMKLTIDHTPERKDEKERIKK 240
QY 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLKTSVIAEPETKRIKLHHADDSFLVLTDDGI 300
DB 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLKTSVIAEPETKRIKLHHADDSFLVLTDDGI 300
QY 301 NFMVNSOEICDFVNOCHDPNEAAHVAHQIAOYGTEDNSTAVVVPFGAWGKYKNSINFS 360
DB 301 NFMVNSOEICDFVNOCHDPNEAAHVAHQIAOYGTEDNSTAVVVPFGAWGKYKNSINFS 360
QY 361 FSRSFASSGRWA 372
DB 361 FSRSFASSGRWA 372
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QY 361 FSRSPASSGRWA 372
Db 361 FSRSPASSGRWA 372

RESULT 9
US-09-973-965-4
; Sequence 4, Application US/09973965
; Patent No. US20020124273A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; TITLE OF INVENTION: Diseases
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,965
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 60/304,775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-965-4

Query Match 100.0%; Score 1951; DB 9; Length 372;
Best Local Similarity 100.0%; Pred. No. 4.3e-205;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60
Db 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60
QY 61 WDNFGIWNDRIDEPIILLPPSIKYGKPIKISLENVGCASQIGKREKEDRDFPAQLTDEV 120
Db 61 WDNFGIWNDRIDEPIILLPPSIKYGKPIKISLENVGCASQIGKREKEDRDFPAQLTDEV 120
QY 121 LYFAVYDGHGGPAAADPCHTHMEKICIMDLLPKENKLETLTLTFLAFLDKAFSSHARLSAD 180
Db 121 LYFAVYDGHGGPAAADPCHTHMEKICIMDLLPKENKLETLTLTFLAFLDKAFSSHARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGPMLTIDHTPERKDEKERIKKC 240
Db 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGPMLTIDHTPERKDEKERIKKC 240
QY 241 GGFVAVNSLQGVHNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHADDSPFLVLTDDGI 300
Db 241 GGFVAVNSLQGVHNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHADDSPFLVLTDDGI 300
QY 301 NFMVNSQICDFVQCHDPNEAAHVAHQIYGTEDNSTAVVVPFGAWGKYKNSINFS 360
Db 301 NFMVNSQICDFVQCHDPNEAAHVAHQIYGTEDNSTAVVVPFGAWGKYKNSINFS 360
QY 361 FSRSPASSGRWA 372
Db 361 FSRSPASSGRWA 372

RESULT 10
US-09-973-941-4
; Sequence 4, Application US/09973941
; Patent No. US2002016465A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
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; TITLE OF INVENTION: Diseases
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,941
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 60/304,775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-941-4

Query Match 100.0%; Score 1951; DB 9; Length 372;
Best Local Similarity 100.0%; Pred. No. 4.3e-205;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60
Db 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60
QY 61 WDNFGIWNDRIDEPIILLPPSIKYGKPIKISLENVGCASQIGKREKEDRDFPAQLTDEV 120
Db 61 WDNFGIWNDRIDEPIILLPPSIKYGKPIKISLENVGCASQIGKREKEDRDFPAQLTDEV 120
QY 121 LYFAVYDGHGGPAAADPCHTHMEKICIMDLLPKENKLETLTLTFLAFLDKAFSSHARLSAD 180
Db 121 LYFAVYDGHGGPAAADPCHTHMEKICIMDLLPKENKLETLTLTFLAFLDKAFSSHARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGPMLTIDHTPERKDEKERIKKC 240
Db 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGPMLTIDHTPERKDEKERIKKC 240
QY 241 GGFVAVNSLQGVHNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHADDSPFLVLTDDGI 300
Db 241 GGFVAVNSLQGVHNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHADDSPFLVLTDDGI 300
QY 301 NFMVNSQICDFVQCHDPNEAAHVAHQIYGTEDNSTAVVVPFGAWGKYKNSINFS 360
Db 301 NFMVNSQICDFVQCHDPNEAAHVAHQIYGTEDNSTAVVVPFGAWGKYKNSINFS 360
QY 361 FSRSPASSGRWA 372
Db 361 FSRSPASSGRWA 372

RESULT 11
US-09-986-992-2
; Sequence 2, Application US/09986992
; Publication No. US20030027308A1
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY D.
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN PHOSPHATASES IDENTIFIED FROM
; TITLE OF INVENTION: GENOMIC SEQUENCING
; FILE REFERENCE: 038602/1277
; CURRENT APPLICATION NUMBER: US/09/986,992
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/246,974
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/208,291
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-986-992-2
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Query Match 100.0%; Score 1951; DB 10; Length 372;
Best Local Similarity 100.0%; Pred. No. 4.3e-205;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSGNQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60
DB 1 MSTAALITLVRSGNQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60

QY 61 WDNFGIWDNRIDEPILLPSIKYKGPDKPISLENVGCASQIGKRKENEDRFPDFAQLTDEV 120
DB 61 WDNFGIWDNRIDEPILLPSIKYKGPDKPISLENVGCASQIGKRKENEDRFPDFAQLTDEV 120

QY 121 LYFAVVDGHHGGAADFCCHTHMEKCIIMDLPEKKNLETLTLLAFLEIDKAFSSHARLSAD 180
DB 121 LYFAVVDGHHGGAADFCCHTHMEKCIIMDLPEKKNLETLTLLAFLEIDKAFSSHARLSAD 180

QY 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
DB 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240

QY 241 GGFVAMNSLGQPHVNGRLAMTRSIGDLDKTSGVIAEPETKRIKLHADDSEFLVLTDDGI 300
DB 241 GGFVAMNSLGQPHVNGRLAMTRSIGDLDKTSGVIAEPETKRIKLHADDSEFLVLTDDGI 300

QY 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQAIQVGTEDNSTAVVVPFGAWGKYKNSSEINFS 360
DB 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQAIQVGTEDNSTAVVVPFGAWGKYKNSSEINFS 360

QY 361 FSRSPASSGRWA 372
DB 361 FSRSPASSGRWA 372

RESULT 12
US-09-371-782-4
; Sequence 4, Application US/09971782
; Publication No. US20030186317A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Heichman, Karen
; APPLICANT: Bartel, Paul L.
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; TITLE OF INVENTION: Diseases
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/971,782
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-371-782-4

Query Match 100.0%; Score 1951; DB 10; Length 372;
Best Local Similarity 100.0%; Pred. No. 4.3e-205;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSGNQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60
DB 1 MSTAALITLVRSGNQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60

QY 61 WDNFGIWDNRIDEPILLPSIKYKGPDKPISLENVGCASQIGKRKENEDRFPDFAQLTDEV 120
DB 61 WDNFGIWDNRIDEPILLPSIKYKGPDKPISLENVGCASQIGKRKENEDRFPDFAQLTDEV 120

QY 121 LYFAVVDGHHGGAADFCCHTHMEKCIIMDLPEKKNLETLTLLAFLEIDKAFSSHARLSAD 180
DB 121 LYFAVVDGHHGGAADFCCHTHMEKCIIMDLPEKKNLETLTLLAFLEIDKAFSSHARLSAD 180
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QY 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
DB 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240

QY 241 GGFVAMNSLGQPHVNGRLAMTRSIGDLDKTSGVIAEPETKRIKLHADDSEFLVLTDDGI 300
DB 241 GGFVAMNSLGQPHVNGRLAMTRSIGDLDKTSGVIAEPETKRIKLHADDSEFLVLTDDGI 300

QY 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQAIQVGTEDNSTAVVVPFGAWGKYKNSSEINFS 360
DB 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQAIQVGTEDNSTAVVVPFGAWGKYKNSSEINFS 360

QY 361 FSRSPASSGRWA 372
DB 361 FSRSPASSGRWA 372

RESULT 13
US-10-311-764-1
; Sequence 1, Application US/10311764
; Publication No. US20040023245A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; AU-YOUNG, Janice K.
; APPLICANT: BAUGHN, Marian R.; DING, Li
; APPLICANT: ELLIOTT, Vicki S.; GANDHI, Ameena R.
; APPLICANT: GRIFFIN, Jennifer A.; HAFALIA, April J.A.
; APPLICANT: KEARNEY, Liam; LEE, Ernestine A.
; APPLICANT: LU, Yan; NGUYEN, Dannie B.
; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Javalaxmi
; APPLICANT: REDDY, Roopa M.; SANJANWALA, Madhusudan M.
; APPLICANT: STEWART, Elizabeth A.; TANG, Y. Tom
; APPLICANT: THORNTON, Michael B.; TRIBOULEY, Catherine M.
; APPLICANT: CHAWLA, Narinder K.; YANG, Junming
; APPLICANT: YAO, Monique G.; YUE, Henry
; TITLE OF INVENTION: PROTEIN PHOSPHATASES
; FILE REFERENCE: PI-0126 USN
; CURRENT APPLICATION NUMBER: US/10/311,764
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/19442
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/212,447
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/213,746
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 60/215,210
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/216,529
; PRIOR FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: US 60/218,080
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/220,117
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040023245A1 8124196CDI
US-10-311-764-1

Query Match 100.0%; Score 1951; DB 16; Length 372;
Best Local Similarity 100.0%; Pred. No. 4.3e-205;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSGNQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60
DB 1 MSTAALITLVRSGNQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60

QY 61 WDNFGIWDNRIDEPILLPSIKYKGPDKPISLENVGCASQIGKRKENEDRFPDFAQLTDEV 120
DB 61 WDNFGIWDNRIDEPILLPSIKYKGPDKPISLENVGCASQIGKRKENEDRFPDFAQLTDEV 120
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Db 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRNEDRDFQAULTDEV 120
Qy 121 LYFAYVDHGGPAAADFCHTHMEKIMDLLPKKXNLETLTLAPLEIDKAFSSHARLSAD 180
Db 121 LYFAYVDHGGPAAADFCHTHMEKIMDLLPKKXNLETLTLAPLEIDKAFSSHARLSAD 180
Qy 181 ATLLTSGTTATVALLRDLGIELVAVSGDSRAILCRKGPMPKLTIDHTPERKDEKERIKK 240
Db 181 ATLLTSGTTATVALLRDLGIELVAVSGDSRAILCRKGPMPKLTIDHTPERKDEKERIKK 240
Qy 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLDLKTSIGVIAEPETKRIKLHHADDSFLVLTDDGI 300
Db 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLDLKTSIGVIAEPETKRIKLHHADDSFLVLTDDGI 300
Qy 301 NFMVNSQIEICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGAWGKYKNSINFS 360
Db 301 NFMVNSQIEICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGAWGKYKNSINFS 360
Qy 361 FSRSPASSGRWA 372
Db 361 FSRSPASSGRWA 372

RESULT 14
US-10-716-488-2
; Sequence 2, Application US/10716488
; Publication No. US20040132155A1
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY D.
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN PHOSPHATASES IDENTIFIED FROM
; FILE REFERENCE: 038602/1277
; CURRENT APPLICATION NUMBER: US/10/716,488
; CURRENT FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/246,974
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/208,291
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-716-488-2

Query Match 100.0%; Score 1951; DB 16; Length 372;
Best Local Similarity 100.0%; Pred. No. 4.3e-205;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVTPCHSTSEPRCSRDPDGGSGSPAT 60
Db 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVTPCHSTSEPRCSRDPDGGSGSPAT 60
Qy 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRNEDRDFQAULTDEV 120
Db 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRNEDRDFQAULTDEV 120
Qy 121 LYFAYVDHGGPAAADFCHTHMEKIMDLLPKKXNLETLTLAPLEIDKAFSSHARLSAD 180
Db 121 LYFAYVDHGGPAAADFCHTHMEKIMDLLPKKXNLETLTLAPLEIDKAFSSHARLSAD 180
Qy 181 ATLLTSGTTATVALLRDLGIELVAVSGDSRAILCRKGPMPKLTIDHTPERKDEKERIKK 240
Db 181 ATLLTSGTTATVALLRDLGIELVAVSGDSRAILCRKGPMPKLTIDHTPERKDEKERIKK 240
Qy 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLDLKTSIGVIAEPETKRIKLHHADDSFLVLTDDGI 300
Db 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLDLKTSIGVIAEPETKRIKLHHADDSFLVLTDDGI 300
Qy 301 NFMVNSQIEICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGAWGKYKNSINFS 360
Db 301 NFMVNSQIEICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGAWGKYKNSINFS 360
Qy 361 FSRSPASSGRWA 372
Db 361 FSRSPASSGRWA 372

RESULT 16
US-10-094-749-1699
; Sequence 1699, Application US/10094749
```

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Qy 301 NFMVNSQIEICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGAWGKYKNSINFS 360
Db 301 NFMVNSQIEICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGAWGKYKNSINFS 360
Qy 361 FSRSPASSGRWA 372
Db 361 FSRSPASSGRWA 372

RESULT 15
US-10-716-489-2
; Sequence 2, Application US/10716489
; Publication No. US20040157306A1
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY D.
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN PHOSPHATASES IDENTIFIED FROM
; FILE REFERENCE: 038602/1277
; CURRENT APPLICATION NUMBER: US/10/716,489
; CURRENT FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/246,974
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/208,291
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-716-489-2

Query Match 100.0%; Score 1951; DB 16; Length 372;
Best Local Similarity 100.0%; Pred. No. 4.3e-205;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVTPCHSTSEPRCSRDPDGGSGSPAT 60
Db 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVTPCHSTSEPRCSRDPDGGSGSPAT 60
Qy 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRNEDRDFQAULTDEV 120
Db 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRNEDRDFQAULTDEV 120
Qy 121 LYFAYVDHGGPAAADFCHTHMEKIMDLLPKKXNLETLTLAPLEIDKAFSSHARLSAD 180
Db 121 LYFAYVDHGGPAAADFCHTHMEKIMDLLPKKXNLETLTLAPLEIDKAFSSHARLSAD 180
Qy 181 ATLLTSGTTATVALLRDLGIELVAVSGDSRAILCRKGPMPKLTIDHTPERKDEKERIKK 240
Db 181 ATLLTSGTTATVALLRDLGIELVAVSGDSRAILCRKGPMPKLTIDHTPERKDEKERIKK 240
Qy 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLDLKTSIGVIAEPETKRIKLHHADDSFLVLTDDGI 300
Db 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLDLKTSIGVIAEPETKRIKLHHADDSFLVLTDDGI 300
Qy 301 NFMVNSQIEICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGAWGKYKNSINFS 360
Db 301 NFMVNSQIEICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGAWGKYKNSINFS 360
Qy 361 FSRSPASSGRWA 372
Db 361 FSRSPASSGRWA 372

RESULT 16
US-10-094-749-1699
; Sequence 1699, Application US/10094749
```

/ Publication No. US20030219741A1

/ GENERAL INFORMATION:

/ APPLICANT: ISOGAI, TAKAO

/ APPLICANT: SUGIYAMA, TOMOYASU

/ APPLICANT: OTSUKI, TEISUJI

/ APPLICANT: WAKAMATSU, AI

/ APPLICANT: SATO, HIROYUKI

/ APPLICANT: ISHII, SHIZUKO

/ APPLICANT: YAMAMOTO, JUN-ICHI

/ APPLICANT: ISONO, YUUKO

/ APPLICANT: HIO, YURI

/ APPLICANT: OTSUKA, KAORU

/ APPLICANT: NAGAI, KEIICHI

/ APPLICANT: IRIE, RYOTARO

/ APPLICANT: TAMECHIKO, ICHIRO

/ APPLICANT: SEKI, NAOHICO

/ APPLICANT: YOSHIKAWA, TSUTOMU

/ APPLICANT: OTSUKA, MOTOKYUKI

/ APPLICANT: NAGAHARI, KENJI

/ APPLICANT: MASUHO, YASUHIKO

/ TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA

/ FILE REFERENCE: 084335/0160

/ CURRENT APPLICATION NUMBER: US/10/094,749

/ PRIOR FILING DATE: 2002-03-12

/ PRIOR APPLICATION NUMBER: 60/350,435

/ PRIOR FILING DATE: 2002-01-24

/ PRIOR APPLICATION NUMBER: JP 2001-329381

/ PRIOR FILING DATE: 2001-09-14

/ NUMBER OF SEQ ID NOS: 3381

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 1699

/ LENGTH: 372

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ US-10-094-749-1699

Query Match

Best Local Similarity 99.9%; Score 1950; DB 15; Length 372;

Matches 371; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60

Db 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60

Qy 61 WDNFGIWDNRIDEPILLPSIKYKGPDKISLENVGCASQIGKRKENEDRFPDFAQLTDEV 120

Db 61 WDNFGIWDNRIDEPILLPSIKYKGPDKISLENVGCASQIGKRKENEDRFPDFAQLTDEV 120

Qy 121 LYFAVYDGHGGPAAADFCHTHMEKIMDLPKKNLETLTLTFLAFLDKAFSSHARLSAD 180

Db 121 LYFAVYDGHGGPAAADFCHTHMEKIMDLPKKNLETLTLTFLAFLDKAFSSHARLSAD 180

Qy 181 ATLLTSGTTATVALLRDGIELVAVSGDSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240

Db 181 ATLLTSGTTATVALLRDGIELVAVSGDSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240

Qy 241 GGFVAVNSLQGHVNGRLAMTRISIGDLTKTSVIAEPETKRIKLHADDSEFLVLTDDGI 300

Db 241 GGFVAVNSLQGHVNGRLAMTRISIGDLTKTSVIAEPETKRIKLHADDSEFLVLTDDGI 300

Qy 301 NFWVNSQEI CDVFNQCHDPNEAAHVAHQAIQYGTEDNSTAVVVPFGANGKYKNSSEINFS 360

Db 301 NFWVNSQEI CDVFNQCHDPNEAAHVAHQAIQYGTEDNSTAVVVPFGANGKYKNSSEINFS 360

Qy 361 FSRSPASSGRWA 372

Db 361 FSRSPASSGRWA 372

RESULT 17

US-10-408-765A-2487

/ Sequence 2487, Application US/10408765A

/ Publication No. US20040101874A1

/ GENERAL INFORMATION:

/ APPLICANT: Ghosh, Soumitra S.

/ APPLICANT: Faby, Eoin D.

/ APPLICANT: Zhang, Bing

/ APPLICANT: Gibson, Bradford W.

/ APPLICANT: Taylor, Steven W.

/ APPLICANT: Glenn, Gary W.

/ APPLICANT: Warnock, Dale E.

/ TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION

/ FILE REFERENCE: 660088.465

/ CURRENT APPLICATION NUMBER: US/10/408,765A

/ CURRENT FILING DATE: 2003-04-04

/ NUMBER OF SEQ ID NOS: 3077

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 2487

/ LENGTH: 372

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ US-10-408-765A-2487

Query Match

Best Local Similarity 99.9%; Score 1950; DB 16; Length 372;

Matches 371; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60

Db 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60

Qy 61 WDNFGIWDNRIDEPILLPSIKYKGPDKISLENVGCASQIGKRKENEDRFPDFAQLTDEV 120

Db 61 WDNFGIWDNRIDEPILLPSIKYKGPDKISLENVGCASQIGKRKENEDRFPDFAQLTDEV 120

Qy 121 LYFAVYDGHGGPAAADFCHTHMEKIMDLPKKNLETLTLTFLAFLDKAFSSHARLSAD 180

Db 121 LYFAVYDGHGGPAAADFCHTHMEKIMDLPKKNLETLTLTFLAFLDKAFSSHARLSAD 180

Qy 181 ATLLTSGTTATVALLRDGIELVAVSGDSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240

Db 181 ATLLTSGTTATVALLRDGIELVAVSGDSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240

Qy 241 GGFVAVNSLQGHVNGRLAMTRISIGDLTKTSVIAEPETKRIKLHADDSEFLVLTDDGI 300

Db 241 GGFVAVNSLQGHVNGRLAMTRISIGDLTKTSVIAEPETKRIKLHADDSEFLVLTDDGI 300

Qy 301 NFWVNSQEI CDVFNQCHDPNEAAHVAHQAIQYGTEDNSTAVVVPFGANGKYKNSSEINFS 360

Db 301 NFWVNSQEI CDVFNQCHDPNEAAHVAHQAIQYGTEDNSTAVVVPFGANGKYKNSSEINFS 360

Qy 361 FSRSPASSGRWA 372

Db 361 FSRSPASSGRWA 372

RESULT 18

US-09-925-300-1655

/ Sequence 1655, Application US/09925300

/ Patent No. US20020151681A1

/ GENERAL INFORMATION:

/ APPLICANT: Craig Rosen,

/ APPLICANT: Steve Ruben,

/ TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

/ FILE REFERENCE: PA101

/ CURRENT APPLICATION NUMBER: US/09/925,300

/ CURRENT FILING DATE: 2001-08-10

/ PRIOR APPLICATION NUMBER: PCT/US00/05988

/ PRIOR FILING DATE: 2000-03-08

/ PRIOR APPLICATION NUMBER: 60/124,270

/ PRIOR FILING DATE: 1999-03-12

/ NUMBER OF SEQ ID NOS: 1890

/ SOFTWARE: PatentIn Ver. 2.0

/ SEQ ID NO 1655

/ LENGTH: 373

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (144)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (290)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (325)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (328)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-945-300-1655

Query Match      98.6%; Score 1924; DB 9; Length 373;
Best Local Similarity 98.9%; Pred. No. 4e-202;
Matches 368; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60
Db 2 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 61
Qy 61 WDNFGIWDNRIDEPIILLPPSIKYGKPIKISLENVGCASQIGKKEKENEDEDFDFAQLTDEV 120
Db 62 WDNFGIWDNRIDEPIILLPPSIKYGKPIKISLENVGCASQIGKKEKENEDEDFDFAQLTDEV 121
Qy 121 LYFVAVDGHGGAADFCFTHMEKICIMDLPEKKNLETLTLAFLEIDKAFSSHARLSAD 180
Db 122 LYFVAVDGHGGAADFCFTHMEKICIMDLPEKKNLETLTLAFLEIDKAFSSHARLSAD 181
Qy 181 ATLLTSGTTATVALLRDGIELVAVSGDSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
Db 182 ATLLTSGTTATVALLRDGIELVAVSGDSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 241
Qy 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHHADDSFLVLTDDGI 300
Db 242 GGFVAMNSLGQPHVNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHHADDSFLVLTDDGI 301
Qy 301 NFVNSQIEICDFVNOCHDPNEAAHVAVTEQAIQYGTEDNSTAVVVPFGAWGKYKNSEINFS 360
Db 302 NFVNSQIEICDFVNOCHDPNEAAHVAVTEQAIQYGTEDNSTAVVVPFGAWGKYKNSEINFS 361
Qy 361 FSRSFASSGRWA 372
Db 362 FSRSFASSGRWA 373

RESULT 19
US-09-850-351-2
; Sequence 2, Application US/09860351
; Patent No. US20020077463A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 16105, A NOVEL PROTEIN HUMAN PHOSPHATASE
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 38155-20013.00
; CURRENT APPLICATION NUMBER: US/09/860,351
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/205,260
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-860-351-2
Query Match      88.5%; Score 1727; DB 9; Length 352;

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Best Local Similarity 99.4%; Pred. No. 1.7e-180;
Matches 330; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60
Db 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60
Qy 61 WDNFGIWDNRIDEPIILLPPSIKYGKPIKISLENVGCASQIGKKEKENEDEDFDFAQLTDEV 120
Db 61 WDNFGIWDNRIDEPIILLPPSIKYGKPIKISLENVGCASQIGKKEKENEDEDFDFAQLTDEV 120
Qy 121 LYFVAVDGHGGAADFCFTHMEKICIMDLPEKKNLETLTLAFLEIDKAFSSHARLSAD 180
Db 121 LYFVAVDGHGGAADFCFTHMEKICIMDLPEKKNLETLTLAFLEIDKAFSSHARLSAD 180
Qy 181 ATLLTSGTTATVALLRDGIELVAVSGDSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
Db 181 ATLLTSGTTATVALLRDGIELVAVSGDSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
Qy 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHHADDSFLVLTDDGI 300
Db 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHHADDSFLVLTDDGI 300
Qy 301 NFVNSQIEICDFVNOCHDPNEAAHVAVTEQAIQ 332
Db 301 NFVNSQIEICDFVNOCHDPNEAAHVAVTEQVTQ 332

RESULT 20
US-10-353-690-44
; Sequence 44, Application US/10353690
; Publication No. US20030215840A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Donoghue, Mary
; APPLICANT: Stagliano, Nancy
; APPLICANT: Perodin, Jacqueline
; APPLICANT: Rodrique-Way, Amelie
; TITLE OF INVENTION: Methods and compositions for treating
; TITLE OF INVENTION: cardiovascular disease using 1692, 6169, 6193, 7771, 14395,
; TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 1720,
; TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
; TITLE OF INVENTION: 14245, 58848, 1870, 25856, 32394, 3484, 345, 9252, 9135,
; TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912, 2868,
; TITLE OF INVENTION: 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914,
; TITLE OF INVENTION: 51130, 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474,
; FILE REFERENCE: MPI02-018P1RNMNIM
; CURRENT APPLICATION NUMBER: US/10/353,690
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 60/353,224
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/364,529
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: 60/373,861
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/376,287
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 60/388,080
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: 60/390,971
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/394,130
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/394,797
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/404,904
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/405,450

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; PRIOR FILING DATE: 2002-08-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-353-690-44

Query Match      88.5%; Score 1727; DB 15; Length 352;
Best Local Similarity 99.4%; Pred. No. 1.7e-180;
Matches 330; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSTAALITLVRSQGNQVRRVLLSSLLQDDRRVPTCHSSSTSEPRCSRFDDGSGSPAT 60
Db 1 MSTAALITLVRSQGNQVRRVLLSSLLQDDRRVPTCHSSSTSEPRCSRFDDGSGSPAT 60
Qy 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRNEDRFDFAQLTDEV 120
Db 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRNEDRFDFAQLTDEV 120
Qy 121 LYFAVYDGHGGPAAADFCHTHMEKIMDLPEKKNLETLTLTAFLIDKAPSSHARLSAD 180
Db 121 LYFAVYDGHGGPAAADFCHTHMEKIMDLPEKKNLETLTLTAFLIDKAPSSHARLSAD 180
Qy 181 ATLLTSGTTATVALLRDGIELVVASVGDSTRILCRKGKPMKLTIDHTPERKDEKERIKK 240
Db 181 ATLLTSGTTATVALLRDGIELVVASVGDSTRILCRKGKPMKLTIDHTPERKDEKERIKK 240
Qy 241 GGFVANNLSGQPHVNGRLAMTRISIGDLTKTSVIAEPETKIKLHHADDSFLVLTDDGI 300
Db 241 GGFVANNLSGQPHVNGRLAMTRISIGDLTKTSVIAEPETKIKLHHADDSFLVLTDDGI 300
Qy 301 NFVNSQECIDFVNQCHDNEAAHAYTEQAIO 332
Db 301 NFVNSQECIDFVNQCHDNEAAHAYTEQVTQ 332

RESULT 21
US-10-094-749-3238
; Sequence 3238, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKANATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; PRIOR FILING DATE: 2002-03-12
; CURRENT APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3238
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; LENGTH: 150
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-3238

Query Match      40.5%; Score 790; DB 15; Length 150;
Best Local Similarity 100.0%; Pred. No. 4.3e-78;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTAALITLVRSQGNQVRRVLLSSLLQDDRRVPTCHSSSTSEPRCSRFDDGSGSPAT 60
Db 1 MSTAALITLVRSQGNQVRRVLLSSLLQDDRRVPTCHSSSTSEPRCSRFDDGSGSPAT 60
Qy 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRNEDRFDFAQLTDEV 120
Db 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRNEDRFDFAQLTDEV 120
Qy 121 LYFAVYDGHGGPAAADFCHTHMEKIM 147
Db 121 LYFAVYDGHGGPAAADFCHTHMEKIM 147

RESULT 22
US-10-072-012-853
; Sequence 853, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerkhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
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; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 854
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Protein
; OTHER INFORMATION: phosphatase 2C Consensus Sequence
US-10-072-012-854

Query Match      20.3%; Score 395.5; DB 12; Length 252;
Best Local Similarity 40.5%; Pred. No. 2.3e-34;
Matches 105; Conservative 41; Mismatches 90; Indels 23; Gaps 9;

QY      94  NVCASQIGKRNED-----RPDFAQLTDEVLVYFAVDGCHGPPAADFCHTHMEK--C 145
Db      2  DVGVSVMQGFPRKPMEDAHIAKGNLNSGGKSGKGFVAFVDGCHGGSQAAYAGKHELTCLA 61
QY      146 IMDLLPKENKLETLTLAFLIEDKAFSSHARLSADATLLTSGTTATVAILRDLGIELVVAS 205
Db      62  LRKSFPELDDLNALXESFLE---STDEELRSSAANTDLDSGSTAVVALLR-GNKLYVAN 117
QY      206 VGDRAILCRKGKPMK-LTIHTPEKDKSKERIKKGGFVAMNSLGQPHVNGRLAMTRSI 264
Db      118 VGDRAVLCRNGNAIKQLTEDHKPNSDEDRRRLEGAGGFVSRNG---RVNGVLAVSRAF 173
QY      265 GDLDLK--TSGVIASPEIKRIKLHHAADSFVLTTDGNFMVNSOEICDFVNAQ--CHDP 319
Db      174 GDFELKGVLPVTPADPVTSHKITFSDE-FLILASDGLMDVLSDQGVVDIVRSSELDGDP 232
QY      320 NEAAHAVTEQAIQYGTEDN 338
Db      233 MEAAEKLVDAIAYGSEDN 251

RESULT 24
US-09-801-267-4
; Sequence 4, Application US/09801267
; Publication No. US20020086296A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 26583, A NOVEL SERINE/THREONINE
; TITLE OF INVENTION: PHOSPHATASE AND USES THEREFOR
; FILE REFERENCE: 10448-025001
; CURRENT APPLICATION NUMBER: US/09/801,267
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: US 60/187,454
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 300
; TYPE: PRT

```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-09-801-267-4

Query Match          19.0%; Score 370.5; DB 12; Length 300;
Best Local Similarity 36.1%; Pred. No. 1.7e-31;
Matches 110; Conservative 39; Mismatches 89; Indels 67; Gaps 12;

QY 94 NVGCASQIGKRNEDRF-----DFAQLTDEVLYFAYVDGHPGPAADFCHTHMEKCI 146
Db 2 DVGVSVMQGWKSMEDAHIALKXNLSSSGKDSWFFAVFDGHS-QAAKYAGKHLHKT 60

QY 147 M---DLLP-----KEKNLETLTLTFLAFLIDKAFSSHARLSADATL-----LTSG 187
Db 61 LAERKSPFGDPWEMKLSLEDALESFLEAD---TDEELRSAAASAANKVLTKEDLSSG 117

QY 188 TTATVALLRDGIELVVASVGDSEALCRKGKPMK----LTIDHTPERKDEKERIKKCGGF 243
Db 118 STAVVALIR-GNKLYVANVGDSRAVLCRNGNAIKWAVLTEDHKPSNEDERERIEAAGGF 176

QY 244 VAWNSLGQPHVNGRLAMTSGIDLDLKTSG-----VIAEPE-TK 281
Db 177 VSRVSNGR--VNGVLAVSRAFGFELKPGSKLGPEESLEANVEYIKSPQLVTAEPDVT 234

QY 282 RIKLHHADSDFLVTTDGINFMVNSQEI CDFV-----NQCHDPNEAAHAHVAITEQAIQY 333
Db 235 STDLTDPKDEFLILACDGLWDVVSDQEVVDIVRSELSGKNKSAEDPMEAAEKLVDDEAIAR 294

QY 334 GTEDN 338
Db 295 GSEDN 299

RESULT 25
US-10-170-789-35
; Sequence 35, Application US/10170789
; Publication No. US20030180930A1
; GENERAL INFORMATION:
; APPLICANT: Rachel E. Meyers
; APPLICANT: Olandt, Peter J.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Williamson, Mark
; APPLICANT: Weich, Nadine
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASE, PHOSPHATASE,
; FILE REFERENCE: 10448-191001
; CURRENT APPLICATION NUMBER: US/10/170,789
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 09/797,039
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06525
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,061
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/882,166
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: PCT/US01/19269
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/212,078
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 09/934,406
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26052
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226,740
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/861,801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PCT/US01/16549
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205,508
```

```
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/801,267
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: PCT/US01/07138
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/187,454
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/829,671
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: PCT/US01/40483
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,508
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/961,721
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/29904
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 60/235,023
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 10/045,367
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/246,561
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: US 09/801,275
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: PCT/US01/07074
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/187,420
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-10-170-789-35

Query Match          19.0%; Score 370.5; DB 14; Length 300;
Best Local Similarity 36.1%; Pred. No. 1.7e-31;
Matches 110; Conservative 39; Mismatches 89; Indels 67; Gaps 12;

QY 94 NVGCASQIGKRNEDRF-----DFAQLTDEVLYFAYVDGHPGPAADFCHTHMEKCI 146
Db 2 DVGVSVMQGWKSMEDAHIALKXNLSSSGKDSWFFAVFDGHS-QAAKYAGKHLHKT 60

QY 147 M---DLLP-----KEKNLETLTLTFLAFLIDKAFSSHARLSADATL-----LTSG 187
Db 61 LAERKSPFGDPWEMKLSLEDALESFLEAD---TDEELRSAAASAANKVLTKEDLSSG 117

QY 188 TTATVALLRDGIELVVASVGDSEALCRKGKPMK----LTIDHTPERKDEKERIKKCGGF 243
Db 118 STAVVALIR-GNKLYVANVGDSRAVLCRNGNAIKWAVLTEDHKPSNEDERERIEAAGGF 176

QY 244 VAWNSLGQPHVNGRLAMTSGIDLDLKTSG-----VIAEPE-TK 281
Db 177 VSRVSNGR--VNGVLAVSRAFGFELKPGSKLGPEESLEANVEYIKSPQLVTAEPDVT 234

QY 282 RIKLHHADSDFLVTTDGINFMVNSQEI CDFV-----NQCHDPNEAAHAHVAITEQAIQY 333
Db 235 STDLTDPKDEFLILACDGLWDVVSDQEVVDIVRSELSGKNKSAEDPMEAAEKLVDDEAIAR 294

QY 334 GTEDN 338
Db 295 GSEDN 299

RESULT 26
US-10-437-963-164347
; Sequence 164347, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
```

APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437.963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 164347
LENGTH: 348
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_63255C.1.pep
US-10-437-963-164347

Query Match 18.9%; Score 369; DB 16; Length 348;
Best Local Similarity 37.5%; Pred. No. 3.2e-31;
Matches 99; Conservative 48; Mismatches 85; Indels 32; Gaps 11;

QY 96 GCASQIGKRNED---RPDFAQLTDEVLYFAYVDGHHGPPAAADFCCHTHMEKICIMDLLP 151
DB 84 GYASAPKGRASMEFYETRIDGVD-GETIGLFGVFDGHHGARAAYVKQL---FSLIK 139
QY 152 KEK---NLETLLTAFLEID----KAFSSHARLSADATLLTSGTTATVALLRDGIELVVA 204
DB 140 HPKIFSDIKSAIAETYNHTSEFLKASSTHTR-----DAGSTASTAIL-VGDRLLVA 190
QY 205 SVGDSRAILCKRGPMLKTIDHTPERKDEKRIKKCGFVAWNSLQPHVNGRLAMTRSI 264
DB 191 NVGSRVAVCGDAIAVSRDEKPDQSDERQRIEDAGGFVW--AGTWVGGVLAVSRAP 248
QY 265 GDLLKTSVIAEPETRIKLHADDSS--FLVLTDTGDNFMVNSQIEICDFVNOCHDNEA 322
DB 249 GDLLKQYVVADPE--IKEEIVDSLEFLILASDGLWDVNSKEAVDWMVRPIQDPEQA 304
QY 323 AHAVTEQAIOYGTEDNSTAVVVPF 346
DB 305 AKRLQEAQYRGSADNTIVVIRF 328

RESULT 27
US-10-424-599-219801
Sequence 219801, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424.599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 219801
LENGTH: 405
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_40508C.1.pep
US-10-424-599-219801

Query Match 18.5%; Score 361; DB 12; Length 405;
Best Local Similarity 31.7%; Pred. No. 3.1e-30;
Matches 97; Conservative 59; Mismatches 98; Indels 52; Gaps 12;

QY 71 IDEPILLPSIKYKPIPKISLNVGCASQIGKRNEDRDFPAQLTD----- 118
DB 81 IEESIETATEF---TPNV---RSGCCADIGRSGMDD--EHIQIDDLAAHLGFVKHP 132
QY 119 -EVLYFAYVDGHHGPPAAADFCCHTHMEKIM---DILLPKE-----KNLETLLTAFLEI 167
DB 133 MSAFAVAFVDFGHHGPPAAAFVKNAMRLLFEDADMLOSVDADALFLKLEDSSHRAFLGA 192
QY 168 KXAFSSHARLSADATLLTSGTTATVALLRDGIELVAVSGDSRAILCKRGPMLKTIDHT 227
DB 193 DLALADEQSVSS-----SCGTTALTALVL-GRHLVAVNAGDCRAVLCRRGVAVDMSQDHR 246
QY 228 PERKDEKRIKKCGFVAWNSLQPHVNGRLAMTRISIGDLDLK-----TSGVIAEPETKR 282
DB 247 PSYLPERRRVEELGGFI-----DDGLNGYLSVTRALGWDWDLKFLPGSASPIADPDVGV 301
QY 283 IKLHADDSSFLVLTDTGDNFMVNSQIEICDFV----NOCHDPNEAAHVAHTQAIOYGTEDN 338
DB 302 VTUTE-DDEFLIIGCDGIDWVSSQDAVSFVRRLRRHDDPQCCARELVKAEALRLHTSDN 360
QY 339 STAVV 344
DB 361 LTIVVI 366

RESULT 28
US-10-424-599-176581
Sequence 176581, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424.599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 176581
LENGTH: 374
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(374)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_130470C.1.pep
US-10-424-599-176581

Query Match 18.5%; Score 360; DB 12; Length 374;
Best Local Similarity 31.6%; Pred. No. 3.5e-30;
Matches 101; Conservative 52; Mismatches 107; Indels 60; Gaps 10;
QY 78 PSIKYKPIPKISLE-----NVGCASQIGKRNEDR 110
DB 28 PPSYRCKLVHRASLQMTKLSDVSAEPHEVTDCCSDFFPMLRSGACTDIGFRSNMEDA 87
QY 111 F-----DEA---QLTDEVLYFAYVDGHHGPPAAADFCCHTHMEKICIMDLLPKEKNLETL 159
DB 88 YVCVDNFMEDYGLKXHDIDGPSAFYGVFDGHHGKHADFACLHLPKEIVDDKDFPDIERI 147
QY 160 LTLAFLEIDKAFSSHARLSADATLLTSGTTATVALLRDGIE---LVAVSGDSRAILCKK 216
DB 148 VASAFIQADNAPAEACSLDA---ALASGTTALTALVIGSFXCRLLVANAGDCRAVLCRR 204
QY 217 GKEMKLTIDHTPERKDEKRIKKCGFVAWNSLQPHVNGRLAMTRISIGD-----LDLKT 271
DB 205 GKAIEMSRDHKPGCKNKKRIEASGSYV-----DGYLNGQLNVARALGDWHEMGKSKD 259


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RESULT 38
US-09-860-351-4
; Sequence 4, Application US/09860351
; Patent No. US20020077463A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals. Inc.
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 16105, A NOVEL PROTEIN HUMAN PHOSPHATASE
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 38155-20013.00
; CURRENT APPLICATION NUMBER: US/09/860,351
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/205,260
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid
US-09-860-351-4

Query Match 17.9%; Score 350; DB 9; Length 274;
Best Local Similarity 36.3%; Pred. No. 2.7e-23;
Matches 104; Conservative 36; Mismatches 73; Indels 74; Gaps 12;

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[illegible]

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Db 352 ADNLTVVVVCF 362

RESULT 40
US-10-425-114-72221
; Sequence 72221, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 72221
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4743-017-A1_FLI.pep
US-10-425-114-72221

Query Match 17.9%; Score 348.5; DB 12; Length 408;
Best Local Similarity 32.8%; Pred. No. 7.4e-29;
Matches 102; Conservative 52; Mismatches 94; Indels 63; Gaps 13;

Qy 87 IPXISLE-----NV--GCASQIGKRKNEED---RFD--FAQLTDEVL 121
Db 64 VPRNGLEQPDVAPSLSTMDIQVFVNRSGSFADIGPRYMEDEHRIDDLHLSHLSMLV 123
Qy 122 -----YFAYVDGHPGAADFCHTIMEKIMD--LLPK-----KNLETLTLTAPL 165
Db 124 CPLPSAFYGVFDGHPGDAAYMKHAMEFLFESEFPQASQVDEYLVESVSCVRRAPL 183
Qy 166 EIDKAFSSHARLSADATLTSGTATVALLRGLIELVWASGDSRAILCRKPKMKLTIID 225
Db 184 QADLALADDLSR-----SSGTTALTALV-FGRQLVWNTGDCRAVLCKKGVAMENSRD 237
Qy 226 HTPERKDEKRIKCGFVWNSLQOPHYNGRLAMTRSIGDLDLKTSG-----VIABPE 279
Db 238 HRANHVEERERVAASGGYTE-----DGYLNGVLSTRALGDMKAPGASASAAALIAEPE 292
Qy 280 TKRILKHHADDSELVLTDTGINFMVNSOICDFV-----NQCHDPNEAAHAYTEQAIQYGT 335
Db 293 FRRTLGE-DDEFLVNGCDGIMDVMTSQHAVSLVRGLRQHDHPARCAKELVMEARLET 351
Qy 336 EDNSTAVVVPF 346
Db 352 ADNLTVVVVCF 362

RESULT 41
US-10-425-114-72766
; Sequence 72766, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 72766
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4762-032-H2_FLI.pep
US-10-425-114-72766

Query Match 17.9%; Score 348.5; DB 12; Length 416;
Best Local Similarity 29.7%; Pred. No. 7.6e-29;
Matches 117; Conservative 51; Mismatches 135; Indels 91; Gaps 13;

Qy 17 VRRVLLSSRLLODDRVTPTCHSSTSEPRCSRFDPDGSGSPATWDFGIMDNRIPEPIL 76
Db 15 VRRKLAVEPPPSLSTLTGFCDSAAVQCCCS-----GRAGGKMGVY-----L 58
Qy 77 LPPSIKYKPIPKISLENVGCASQIGKRKNEEDRDFQAQLTDE-VLYFAYVDGHPGAAA 135
Db 59 STPKTKLSADGENSRVRFGLSSMQGWRITMEDAHAALPDLDECTSFYGVYDGHGKAYS 118
Qy 136 DFCHTHMEKIMDLLPKENY----LETLLTLAFLIEDKAFSSHARLSADATLL----- 184
Db 119 KFCARHLHK---QVLINDANSSGDLPTSLHKAFLRDEMVMKGO-RGWRLELTGDKGNTI 174
Qy 185 -----TSGTTATVALLRGLIELVWASVGD 208
Db 175 SGMIDDIWPKGDSDKIREDWDTBEGPNSNFPPTSGSTACVAVIRND-KLIVANAGD 233
Qy 209 SRAILCRKPKMKLTIDHTPERKDEKRIKCGFVWNSLQOPHYNGRLAMTRSIGDLD 268
Db 234 SRCVISRKGQAYNLSTDKPKDLEERERILGAGGFV-----AGRVNASLNSRAIGDME 288
Qy 269 LKTSG-----VIABPETRIKLHADDSELVLTDTGINFMVNSOICDFVNOCHDPN 320
Db 289 LKQNDLLPVERQIVTAPELKTQLSE-DDEFIVLACDGIWDCMSQEVVDFVHKQLKTE 347
Qy 321 EAAHAYTEQAIQ-----YCTE--DNSTAVVVPF 346
Db 348 DKISSVCEKLLNRCVAPTSGGEGCDNMTVIVQF 381

RESULT 42
US-10-424-599-191145
; Sequence 191145, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 191145
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_14622C.1.pep
US-10-424-599-191145

Query Match 17.8%; Score 347.5; DB 12; Length 383;
Best Local Similarity 34.3%; Pred. No. 8.6e-29;
Matches 93; Conservative 51; Mismatches 94; Indels 33; Gaps 8;

Qy 99 SQIGKRKNEED-----RFDFAQLTDEVL-YFAYVDGHPGAAADFCHTHMEKIM 147
Db 90 SDIGDRTSMEETHICIGDLAEKFGNNELCKEALSFYGVFDGHGKSAAQFVRDHLPRVIV 149

```

QY 148 DLLPKENLETLTAFLEIDKAFSSHARLSADATLTSCTTATVALLRDGIELVVASVG 207
Db 150 EDADFPLEKVVTRSFLEIDAEF--ARSCSTESSLSGTTALTALII-FGRSILLVANAG 205
QY 208 DSRAILCRKGPMLTIDHTPERKDEKRIKCGGFVAMNSLQGPVNGRLATRSIGDL 267
Db 206 DCRAVLSRGGAIEMSKDHRRPLOTCKERKIESLGGYI-----DDGYLNGOLGVTRALGDW 260
QY 268 DL-----KTSGVIAEPETKRIKLHADDSEFLVLTDTGDNFMVNSQIEICDF-----VNO 315
Db 261 HLOQMKINGKGPISAEPELKLTIL-TKDEFLIIGSDGWDVFRSONAVDFARRLQE 319
QY 316 CHDPNEAAHVAEQAIQYGTEDNSTAVVVPF 346
Db 320 HNDVKQCCKEVIGAEIRKRGATDNLTVVMICF 350
RESULT 43
US-10-425-114-70158
; Sequence 70158, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 70158
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73078B07_FLI.pep
US-10-425-114-70158
Query Match 17.8%; Score 346.5; DB 12; Length 360;
Best Local Similarity 31.2%; Pred. No. 1e-28;
Matches 105; Conservative 58; Mismatches 119; Indels 55; Gaps 12;
QY 52 PDGS-----GSPATWDFGNWRDEPILLPS-----IKYKPIPKISL 92
Db 2 PDGYMVCVEEPKDAERFGDPGVVEPAKFPAQMERVCENTTSADPFQKLSNFVPI-- 59
QY 93 ENVGCASOIGKRKENED-----RFDFQAQLTDEVL-YFAVYDGHGGPAAADFCHTH 141
Db 60 -RSGDWSDIGGQYMEDTHVCIPLAKNFGPPLDNEVSYGVYDFDGHGGKDAHFVCDN 118
QY 142 MEKCIIMDLLPKENLETLTAFLEIDKAFSSHARLSADATLTSCTTATVALLRDGIEL 201
Db 119 LPRMIVEDSDPFLQLEKVVTRSFLEIDAEF--ARSCSTESSLSGTTALTALII-FGRSILLVANAG 205
QY 202 VVASVGDSPAILCRKGPMLTIDHTPERKDEKRIKCGGFVAMNSLQGPVNGRLAMT 261
Db 175 LVANAGDCRAVLSRGTAVEMSNDRPCSLSEKLKRVESLGGYV-----DDGYLNGOLGV 229
QY 262 RSIGDL-----KTSGVI-AEPTKRIKLHADDSEFLVLTDTGDNFMVNSQIEICDF- 312
Db 230 RALGDWHLEGMKGAGETGGPLSADPELKWTL-TKDEFLIIGSDGWDVFRSONAVDFARRLQE 319
QY 313 ---VNOCHDPNEAAHVAEQAIQYGTEDNSTAVVVPF 346
Db 289 RKELQEHNDVKLCREIVEEAIKRGATDNLTAIVLVSF 353
RESULT 44
US-10-437-963-157517

; Sequence 157517, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 157517
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_57080C.1.pep
US-10-437-963-157517
Query Match 17.8%; Score 346.5; DB 16; Length 388;
Best Local Similarity 32.6%; Pred. No. 1.1e-28;
Matches 94; Conservative 55; Mismatches 98; Indels 41; Gaps 10;
QY 82 KYGKPIPKISLNVGCASOIGKRKENED-----RFDFQAQLTDEVL-YFAVYDGHG 130
Db 84 KSGNFVPI---RSGDWSDIGGQYMEDTHVCIPLAKNFGQSVNDNEAISFYGVDFDGHG 140
QY 131 GPAADPFCHTHMEKCIIMDLLPKENLETLTAFLEIDKAFSSHARLSADATLTSCTT 190
Db 141 GKDAHFVRDNLPRILVEDADPFLEKVVTRSFVHADNQFAK-----TTLSGTTA 192
QY 191 TVALLRDGIELVVASVGDSPAILCRKGPMLTIDHTPERKDEKRIKCGGFVAMNSLG 250
Db 193 LTAMI-FGRITLLIANAGDCRAVLSRGTAVEMSNDRPCSLSEKLKRVESLGGYV-----D 246
QY 251 QFVNGRLAMTRSIGDL-----KTSG-----VIAPETKRIKLHADDSEFLVLTDTGINF 302
Db 247 DGYLNGOLGVTRALGDWHLEGMKGAGETGGPLSADPELKWTL-TKDEFLIIGSDGWD 305
QY 303 MVNSQIEICDF---VNOCHDPNEAAHVAEQAIQYGTEDNSTAVVVPF 346
Db 306 VFSQNQVDFARRLQEHNDVKSCREIVEEAIKRGATDNLTAIVLVSF 353
RESULT 45
US-10-424-599-219869
; Sequence 219869, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 219869
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_4056C.1.pep
US-10-424-599-219869


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; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 67269
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
;   OTHER INFORMATION: Clone ID: LIB4759-022-G10_F11.psp
US-10-425-114-67269

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Query Match	17.7%	Score	345.5;	DB	12;	Length	343;
Best Local Similarity	33.0%;	Pred.	No. 1.2e-28;				
Matches	92;	Conservative	59;	Mismatches	109;	Indels	19;
Gaps	9						
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Db	56	PPALASRLRTEPIGRSV	DGTLCNGYSSPRGRASMEFDYDIKAKIDDKQINLF	GIPID	115		
QY	128	GGHGPAADFCHTHNEK	CIMDLLPXEKNLETLLTLAFLBTDKAFSSHARLSADA	TLLITSG	187		
		:::::	:::::	:::::	:::::	:::::	
Db	116	GGHGSRAAEYLKEHLF	FENIMKHPEFMNTKLALUSETRYKTDSSEFLDAER----	NTHRDDG	171		
QY	188	TTATVALLARDGIELVA	VASGVDSRAILCRKGKPMKLTIDHTPERKDPERIKKGCGFVAMN	247			
		:::::	:::::	:::::	:::::	:::::	
Db	172	STATAVM-VADHLVAN	VAGVDSRAVISKAGKAIALSEDHKPNRSDEMRNESAGGIVM-	229			
QY	248	SUGCPHVNRGLAWTSI	IGDLTKSGVIABPETRIKLHHADDSDFAVLTTDDGINFNWNSQ	307			
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Db	230	-AGTRWVGVLANSRAF	GNRLK-QPVIADEIQEQINE-ELEFLIIASDGLNDWVSNE	286			
QY	308	EICDFVNQCHPNEAAH	AVTQAIOYGTEDNSTAVVVVF	346			
Db	287	DAVTLVKMEEEPEAAAR	KLTTETAFSRSGDNITCIVKF	325			
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RESULT 49
US-10-424-599-226401
; Sequence 226401, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 226401
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_4646C.1.pep
US-10-424-599-226401

	Query Match	17.6%	Score 344;	DB 12;	Length 338;
	Best Local Similarity	35.6%;	Pred. NO. 1.7e-28;		
	Matches 94;	Conservative 49;	Mismatches 89;	Indels 32;	Gaps 10;
Qy	96	GCAQIGKKENEDRFD--FAQLTDEVL-YEAVVDGHHGPPAAADPCHTHMEKICIMDLDPK	152		
Db	81	GYASSPGKRSMEDPYETKIDGVGEIVGLEFVFDGHHGAAAEYVKONL--- <td>137</td> <td></td> <td></td>	137		
Qy	153	EKNLETLTLTFLAFLDKAFSSHARLSADATLLTS-----GTTATVALLRDGIELVVA	204		
Db	138	PK-----FISDTKSAIDAYNHTDSEFLKSNQNRDAGSGTASTAIL-VGDRLIVA	187		
Qy	205	SVGDSRAILCRKGPMMKLTIDHTPPEKDEKERIKKCGGFVAWNSLGQPHVNGRIAMTRSI	264		
Dp	188	NVGDSRAVICRGGAIAVSROHKPQDTPERRRIEDAGGFVWM--AGTRVGGVLAVSRAF	245		

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QY 265 GDLDTKTSVIAEPETKRIKLHADD$--FLVLTDDGTFNFMVNSQBIICDFVNOCHDPNEA 322
Db 246 GDRLLL-QYVADPEIQESKV---DSSLEFLILASDGLWDVVSNEEAVAMIKPIEDAEA 301
QY 323 AHAVTQAIQYGTEDNSTAVVVPF 346
Db 302 AKELMQEAYQRGSSDNIITCVVVPF 325

RESULT 50
US-10-424-599-226412
; Sequence 226412, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovacic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(63223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 226412
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_4647C.1.pep
US-10-424-599-226412

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Query Match.	17.6%;	Score 344;	DB 12;	Length 338;
Best Local Similarity	35.6%;	Pred. No. 1.7e-28;		
Matches 94; Conservative	49;	Mismatches 89;	Indels 32;	Gaps 10;
Qy	96	GCASQIGKRKENEDRFD--FAQLTDEVL-YFAVVDGHHGGPAAADFCHTHMEKCMIDLPLK	152	
Db	81	GYASSPKRRSMEDFYETKIDGVDGEIVGLFGVFDGHHGGAFAAEVYKQNL--F--PSNLISH	137	
Qy	153	EKNLETLTLTAFLEIDKAPSSHARLSADATILTS-----GTTATVALLRDGIELVVA	204	
Db	138	PK-----FISDTKSAIDAYNVHTDSBFLKSENNQNQRNDAGSTASTAIL--VGDRLILVA	187	
Qy	205	SVGDSRAILCRKGKFMKLITDHTPERXDEKERIKKCGGFVAWNSLGGPHVNGRLAMTRSI	264	
Db	188	NVGDSRAVICRGGNAIAVSRDHKPDQTDERRRIEDAGGFVNW--AGTWRVGGVLAVSRAF	245	
Qy	265	GLDLKTSYGIABETKRIKLHADD--FLVLTDDGINFMVNSQEIICDFVYNQCHDPNEA	322	
Db	246	GDRLUK-QYVVDPEIQEEKV---DSSLLEFLLASDGLWDVVVNEEAAMIKPIEDAEAA	301	
Qy	323	AHAVTEQAQYGTEDNSTAVVVPF	346	
Db	302	AKRLMOEAYORGSSDNITCVVVR	325	

Search completed: October 17, 2004, 15:23:48
Job time : 97 secs

Blank

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 12, 2004, 05:55:18 ; Search time 105 Seconds
(without alignments)
182.903 Million cell updates/sec

Title: US-10-716-488-2
Perfect score: 1951
Sequence: 1 MSTAALITLVRSQGNQVRR.....KNSBINFSSRSPASSGRWA 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1951	100.0	372	4	US-09-973-963-4
2	325	16.7	281	2	US-08-822-701-9
3	325	16.7	281	3	US-08-935-855-9
4	319.5	16.4	390	2	US-08-873-093-3
5	319.5	16.4	390	4	US-09-206-646-3
6	314	16.1	392	3	US-09-013-881-2
7	314	16.1	392	4	US-09-612-473-2
8	307.5	15.8	390	4	US-09-206-646-4
9	306.5	15.7	306	2	US-08-822-701-8
10	306.5	15.7	306	3	US-08-935-855-8
11	300	15.4	309	2	US-08-822-701-7
12	300	15.4	309	3	US-08-935-855-7
13	282.5	14.5	478	2	US-08-873-093-1
14	282.5	14.5	478	2	US-08-873-093-4
15	282.5	14.5	479	4	US-09-206-646-1
16	281.5	14.4	387	4	US-09-461-325-178
17	281.5	14.4	387	4	US-10-012-542-178
18	279	14.3	314	2	US-08-822-701-10
19	279	14.3	314	3	US-08-935-855-10
20	228.5	11.7	542	3	US-08-935-855-20
21	226	11.6	546	3	US-08-935-855-20
22	223	11.4	392	2	US-08-822-701-2
23	223	11.4	392	3	US-08-935-855-2
24	197.5	10.1	1874	4	US-09-331-403-2
25	176.5	9.0	504	2	US-08-752-891-6
26	176.5	9.0	504	2	US-09-144-178-6
27	176.5	9.0	504	3	US-09-406-854-6

ALIGNMENTS

RESULT 1

US-09-973-963-4
; Sequence 4, Application US/09973963
; Patent No. 6653102
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; TITLE OF INVENTION: Protein-Protein Interactions in ND
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,963
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 60/304,775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-963-4

Query Match 100.0%; Score 1951; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 5.3e-193;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSTAALITLVRSQGNQVRRVLLSSRLLODRVPTCHSSTSEPRCSRFPDGGSPAT	60
Db	1	MSTAALITLVRSQGNQVRRVLLSSRLLODRVPTCHSSTSEPRCSRFPDGGSPAT	60
QY	61	WDNFGIWDNRIDPILPPSIKYGKPIPKTSLENVGCASQIGKRKENEFRDFAQLTDEV	120
Db	61	WDNFGIWDNRIDPILPPSIKYGKPIPKTSLENVGCASQIGKRKENEFRDFAQLTDEV	120
QY	121	LYFAVYDGHGGAADFCHTHMEKCMIDLPPKKNLTLLTFLAFLEIDKAFSSHARLSAD	180
Db	121	LYFAVYDGHGGAADFCHTHMEKCMIDLPPKKNLTLLTFLAFLEIDKAFSSHARLSAD	180
QY	181	ATLTSQTTATVALLRDGIELVVASVGDSSRAILCRKGPKMLTIDHTPERKDEKERIKK	240
Db	181	ATLTSQTTATVALLRDGIELVVASVGDSSRAILCRKGPKMLTIDHTPERKDEKERIKK	240
QY	241	GGFVAVNSLQGFVNGRLANTRISIGDLDTKTSVIAEPETKRIKLHADDSEFLVITDGI	300
Db	241	GGFVAVNSLQGFVNGRLANTRISIGDLDTKTSVIAEPETKRIKLHADDSEFLVITDGI	300
QY	301	NFMVNSQEICDFVNOCHDPNEAAHAHVTEQAIQYGTEDNSTAVVVPFGAWGKYKNSEINF	360

QY 344 V 344
DB 279 V 279

RESULT 4

US-08-873-093-3
; Sequence 3, Application US/08873093
; Patent No. 5853997
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,093
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0319 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1247927
US-08-873-093-3

Query Match 16.4%; Score 319.5; DB 2; Length 390;
Best Local Similarity 31.6%; Pred. No. 2.3e-24;
Matches 94; Conservative 48; Mismatches 108; Indels 47; Gaps 10;
QY 88 PKISLENV-----GCASQIGKXKXENEDR-----FDFAQLTDEVLYFAVYDGHGGPAA 134
DB 8 PKTEKHNAHCAGNGLRYGLSSMQGWVEMEDAHAVVGIPHGLEDWSFFAVYDGHAGSRV 67
QY 135 ADFCHTHM-----EKCIMDLLPKENKLETLTLAFLAIDKAFSSHARLSADA 181
DB 68 ANYCSTHLEHTTNEEDFRAADKSGFALEFSVENVKTGIRGTGLKIDYMRNFSDLRNG- 126
QY 182 TLLTSGTTATVALLRDGIELVVASGDSRAILCRKPKMKLTIDHTPERKDEKRIKKG 241
DB 127 -MDRSGSTA-VGVMISPTHIYFINGDGSRAVLCRNGQVCFSTQDHPKCPNMEKRIQAG 184
QY 242 GFVAMNSLGQPHVNGRLAMTRISGIDLK-----TSGVIA-EPETKRIKLHADDNFL 293
DB 185 G-----SVMIQRVNGSLAVSRALGDYDKVCDGKGPTEQLVSPPEVYEI-LRAEEDFV 238

US-08-873-093-3

QY 294 VLTDDGINFMVNSQEIFCDFVQ-----CHDPNEAAHAHVTEQAIOYGTEDNSTAVVVPF 346
DB 239 VLACDGIWDMVMSNEELCFVNSRLVSDDDLENVCNWWVDTCILHKGRDMSIVLVCF 295

RESULT 5

US-09-206-646-3
; Sequence 3, Application US/09206646
; Patent No. 6436637
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
; FILE REFERENCE: PF-0319-1 DIV
; CURRENT APPLICATION NUMBER: US/09/206,646
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: ID No. 6436637 g247927
US-09-206-646-3

Query Match 16.4%; Score 319.5; DB 4; Length 390;
Best Local Similarity 31.6%; Pred. No. 2.3e-24;
Matches 94; Conservative 48; Mismatches 108; Indels 47; Gaps 10;
QY 88 PKISLENV-----GCASQIGKXKXENEDR-----FDFAQLTDEVLYFAVYDGHGGPAA 134
DB 8 PKTEKHNAHCAGNGLRYGLSSMQGWVEMEDAHAVVGIPHGLEDWSFFAVYDGHAGSRV 67
QY 135 ADFCHTHM-----EKCIMDLLPKENKLETLTLAFLAIDKAFSSHARLSADA 181
DB 68 ANYCSTHLEHTTNEEDFRAADKSGFALEFSVENVKTGIRGTGLKIDYMRNFSDLRNG- 126
QY 182 TLLTSGTTATVALLRDGIELVVASGDSRAILCRKPKMKLTIDHTPERKDEKRIKKG 241
DB 127 -MDRSGSTA-VGVMISPTHIYFINGDGSRAVLCRNGQVCFSTQDHPKCPNMEKRIQAG 184
QY 242 GFVAMNSLGQPHVNGRLAMTRISGIDLK-----TSGVIA-EPETKRIKLHADDNFL 293
DB 185 G-----SVMIQRVNGSLAVSRALGDYDKVCDGKGPTEQLVSPPEVYEI-LRAEEDFV 238

US-09-206-646-3

RESULT 6

US-09-013-881-2
; Sequence 2, Application US/09013881
; Patent No. 6132964
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto

US-09-013-881-2

```

; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/013,881
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BILLINGS, LUCY J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0470 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 392 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KIDNOT02
; CLONE: 195647
; US-09-013-881-2

Query Match 16.1%; Score 314; DB 3; Length 392;
Best Local Similarity 27.5%; Pred. No. 8.6e-24;
Matches 110; Conservative 56; Mismatches 120; Indels 114; Gaps 15;

QY 27 LLODDRVTCHSTSEPRCSRDPDGGSPATWDFGWDNRIDEPILLPPSI----- 81
Db 27 LLFDD---LPPASSTDS-----GSGPLLFDD-----LPPASGGDSG 60

QY 82 -----KYPKISLNVGCASQIGKRK-ENED 109
Db 61 SLATSIQVMVTEKGAKRTSEEEKNGSEELVEKKVKCRASSVIFGLKGVAERKGEREE 120

QY 110 RFD-----FAQLTDE-----VLYFAYDGGHGGPAAADFCHTHMEKIMDLPLK--- 152
Db 121 MQDAHVLNDITECRPPSSSLITRVSYFAVFDGGHGGIRASKFAAQNHLQNLIRKPKGDV 180

QY 153 ---EKNLETLTLTFLAFLIDKAFSSHARLSADATLLTSGTTATVALLRDGIELVWASVGS 209
Db 181 ISVEKIVKRCLLDTFKHTDDEFLKQA--SSQKPAWKDGGSTATCVLAVDNI-IYIANLGDS 237

QY 210 RAILCR-----KGKPMKLTIDHTPERKDEKERIKKCGGFVAMNSLGQPHVNGRLAMTRS 263
Db 238 RAILCRYNESQKHAALSLSKEHNPTQYERMEIRKAGG-----NVRDGRVLGVLEVSRS 292

QY 264 IGDLDLKTSGVIAPEPKRIKLHADDSEFLVLTDDGINFMWNSOEICDFVNOCHDNE-- 321
Db 293 IGDQYKRCGVTSVPDIRRCQL--TPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQ 351

QY 322 -----AAHAVTEQAIOYGTEDNSTAVVVPFG 347
Db 352 TREKSAADARYEAACNRLANKAVQGSADNVTVWVRIG 391

RESULT 7
US-09-612-473-2
; Sequence 2, Application US/09612473
; Patent No. 6518029
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga

```

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; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
; FILE REFERENCE: PF-0470-1 CIP
; CURRENT APPLICATION NUMBER: US/09/612,473
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/013,881
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6518029 195647
; US-09-612-473-2

Query Match 16.1%; Score 314; DB 4; Length 392;
Best Local Similarity 27.5%; Pred. No. 8.6e-24;
Matches 110; Conservative 56; Mismatches 120; Indels 114; Gaps 15;

QY 27 LLODDRVTCHSTSEPRCSRDPDGGSPATWDFGWDNRIDEPILLPPSI----- 81
Db 27 LLFDD---LPPASSTDS-----GSGPLLFDD-----LPPASGGDSG 60

QY 82 -----KYPKISLNVGCASQIGKRK-ENED 109
Db 61 SLATSIQVMVTEKGAKRTSEEEKNGSEELVEKKVKCRASSVIFGLKGVAERKGEREE 120

QY 110 RFD-----FAQLTDE-----VLYFAYDGGHGGPAAADFCHTHMEKIMDLPLK--- 152
Db 121 MQDAHVLNDITECRPPSSSLITRVSYFAVFDGGHGGIRASKFAAQNHLQNLIRKPKGDV 180

QY 153 ---EKNLETLTLTFLAFLIDKAFSSHARLSADATLLTSGTTATVALLRDGIELVWASVGS 209
Db 181 ISVEKIVKRCLLDTFKHTDDEFLKQA--SSQKPAWKDGGSTATCVLAVDNI-IYIANLGDS 237

QY 210 RAILCR-----KGKPMKLTIDHTPERKDEKERIKKCGGFVAMNSLGQPHVNGRLAMTRS 263
Db 238 RAILCRYNESQKHAALSLSKEHNPTQYERMEIRKAGG-----NVRDGRVLGVLEVSRS 292

QY 264 IGDLDLKTSGVIAPEPKRIKLHADDSEFLVLTDDGINFMWNSOEICDFVNOCHDNE-- 321
Db 293 IGDQYKRCGVTSVPDIRRCQL--TPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQ 351

QY 322 -----AAHAVTEQAIOYGTEDNSTAVVVPFG 347
Db 352 TREKSAADARYEAACNRLANKAVQGSADNVTVWVRIG 391

RESULT 8
US-09-206-646-4
; Sequence 4, Application US/09206646
; Patent No. 6436637
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Lal, Preeti G.
; APPLICANT: Corley, Neil C.
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
; FILE REFERENCE: PF-0319-1 DIV
; CURRENT APPLICATION NUMBER: US/09/206,646
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 390

```

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/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: ID No. 6436637 g452526
US-09-206-646-4

Query Match      15.8%; Score 307.5; DB 4; Length 390;
Best Local Similarity 31.0%; Pred. No. 4e-23;
Matches 92; Conservative 48; Mismatches 110; Indels 47; Gaps 10;

QY 88 PKISLENV-----GCASQIGKKEKEDR-----FDFALQTLDEVLYFAVYDGHGGPAA 134
Db 8 PKTEKINAGAGNGLRYGLSSWQGWVEMEDAHTAVVGIPHLGNDWNSFFAVYDGHAGSRV 67
QY 135 ADFCHTHM-----EXCIMDLLPKKLETLTLTFLAFLDK--AFSSSHARLSADA 181
Db 68 ANYCSTHLEHITNEDFRAADKSGSALSPSVESVKTGRTGFLKIDYMRNFDLRNG- 126
QY 182 TLLTSTATTALLRDGIELVWASVDSRAILCRKGPMLTIDHTPERKDEKERIKKCG 241
Db 127 -MDRSSTA-VGVWVSPTHMYFINGDSRAVLCRNGQVCFSTQDHKPCNPFVEKERIQNAG 184
QY 242 GFVAMNSLQCPHYNGRLAMTRSGIDLK-----TSGVIA-EPETKRIKLHADDGFL 293
Db 185 G-----SVMIQRYNGSLAVSRALGDYDKVDGKGPTEQLVSPPEVYEL-VRAEEDFV 238
QY 294 VLTDTGINFWNSQIECDFVQ-----CHDPNEAAHVAETQAIQYGTEDNSTAVVVPF 346
Db 239 VLACDGIWVNGNEELCEEFVRSRLEVSDLENVCNVWVDTCLHKGSRDNMSVVLVCF 295

RESULT 9
US-08-822-701-8
/ Sequence 8, Application US/08822701
/ Patent No. 5976853
/ GENERAL INFORMATION:
/ APPLICANT: Guthridge, Mark
/ APPLICANT: Basilio, Claudio
/ TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
/ TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: David A. Jackson, Esq.
/ STREET: 411 Hackensack Ave, Continental Plaza, 4th
/ CITY: Hackensack
/ STATE: New Jersey
/ COUNTRY: USA
/ ZIP: 07601
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/822,701
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Jackson Esq., David A.
/ REGISTRATION NUMBER: 26,742
/ REFERENCE/DOCKET NUMBER: 1049-1-002 N
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201-487-5800
/ TELEFAX: 201-343-1684
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 306 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
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/ HYPOTHETICAL: NO
/ FRAGMENT TYPE:
/ ORIGINAL SOURCE:
/ ORGANISM: Rattus
US-08-822-701-8

Query Match      15.7%; Score 306.5; DB 2; Length 306;
Best Local Similarity 31.0%; Pred. No. 3.5e-23;
Matches 91; Conservative 43; Mismatches 115; Indels 45; Gaps 10;

QY 88 PKISLENV-----GCASQIGKKEKEDR-----FDFALQTLDEVLYFAVYDGHGGPAA 134
Db 8 PKTEKINAGAGNGLRYGLSSWQGWVEMEDAHTAVGILSPSGLETWGFVAVYDGHAGSOV 67
QY 135 ADFCHTHMCKIMDL-----LPKEKNLETLTLTFLAFLDK--AFSSSHARLSADATLL 184
Db 68 AKYCCHELLDHI TNQDPFKGSAGAPSVENKNGRTGFLBIDEHMRVMSKKGAD---- 123
QY 185 TSGTATTALLRDGIELVWASVDSRAILCRKGPMLTIDHTPERKDEKERIKKCGFV 244
Db 124 RSGSTA-VGVLISSPQHTYFINGDSRGLLCRNKRVHFTQDHKPSNPLEKRIQNAG-- 180
QY 245 AWMISLQCPHYNGRLAMTRSGIDLK-----TSGVIA-EPETKRIKLHADDGFLVLT 296
Db 181 ---SVMIQRYNGSLAVSRALGDYDKVDGKGPTEQLVSPPEVYEL-VRAEEDFV 237
QY 297 TDGINFWNSQIECDFVQ-----CHDPNEAAHVAETQAIQYGTEDNSTAVVVPF 346
Db 238 CDGIWVNGNEELCDFVRSRLEVSDLENVCNVWVDTCLHKGSRDNMSVILICF 291

RESULT 10
US-08-935-855-8
/ Sequence 8, Application US/08935855
/ Patent No. 6066485
/ GENERAL INFORMATION:
/ APPLICANT: Guthridge, Mark
/ APPLICANT: Basilio, Claudio
/ TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
/ TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: David A. Jackson, Esq.
/ STREET: 411 Hackensack Ave, Continental Plaza, 4th
/ CITY: Hackensack
/ STATE: New Jersey
/ COUNTRY: USA
/ ZIP: 07601
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/935,855
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Jackson Esq., David A.
/ REGISTRATION NUMBER: 26,742
/ REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201-487-5800
/ TELEFAX: 201-343-1684
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 306 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
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; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Rattus
US-08-935-855-8

Query Match 15.7%; Score 306.5; DB 3; Length 306;
Best Local Similarity 31.0%; Pred. No. 3.5e-23;
Matches 91; Conservative 43; Mismatches 115; Indels 45; Gaps 10;

QY 88 PKISLENY-----GCASQIGKRENEDEDR-----PDFAQLTDEVLYFAVYDGHGPPAA 134
DB 8 PKMEKHNAQGGNGRLRYGLSSQGWVRVEMEDAHAVVGVIPHGLDNWGSFFAVYDGHAGSQV 67
QY 135 ADPCHTMEKIMDL-----LPKEKNLETLTLAFLAIDK--AFSSSHARLSADATLL 184
DB 68 AKYCEHLLDHTNNQDFKGSAGAPSVENVKNGIRGTGFLAIDEMRVMSKKHGAD----- 123
QY 185 TSGTTATVALLRDGIELVAVSGDSRAILCRKKGPKMLTIDHTPERKDEKERIKKCGFV 244
DB 124 RSGSTA-VGVLISSPQHTYFVINGDSRGLLCRNKRVHFFTDHKPSPLEKRIQNAGG-- 180
QY 245 AWMNSLGQPHVNGRLAMTRISIGDLK-----TSGVIA-EPETKRIKLHADDSEFLVLT 296
DB 181 ---SVMIQKRVNGSLAVSRALGDFYKCVHGKQTEQLVSPPEVHDIERSEEDDQFIILA 237
QY 297 TDGINFMVNSQIEICDFVQ-----CHDPNEAAHAYTEQAIQYGTEDNSTAVVVPF 346
DB 238 CDGIWDMVNGNEELCDFVRSRLVETDLDLEKVCNEVVDTCLYKGRDNMSVILICF 291

RESULT 11
US-08-822-701-7
; Sequence 7, Application US/08822701
; Patent No. 5976853
; GENERAL INFORMATION:
; APPLICANT: Guthridge, Mark
; APPLICANT: Basilio, Claudio
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,701
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-002 N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:

; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-822-701-7

Query Match 15.4%; Score 300; DB 2; Length 309;
Best Local Similarity 31.3%; Pred. No. 1.7e-22;
Matches 93; Conservative 47; Mismatches 109; Indels 48; Gaps 11;

QY 88 PKISLENY-----GCASQIGKRENEDEDR-----PDFAQLTDEVLYFAVYDGHGPPAA 134
DB 8 PKTEKHNAHAGNGRLRYGLSSQGWVRVEMEDAHAVVGVIPHGLDNWGSFFAVYDGHAGSRV 67
QY 135 ADPCHTMEKIMDL-----LPKEKNLETLTLAFLAIDK--AFSSSHARLSADATLL 181
DB 68 ANYCSTHLEHITTTNEDFRAADKSGSALPESVSVKTKTGT--GFLKIDYEMRNFSDLRNG-- 125
QY 182 TLTSTGTTATVALLRDGIELVAVSGDSRAILCRKKGPKMLTIDHTPERKDEKERIKKCG 241
DB 126 -MDRSGSTA-VGVWVSPHMYFVINGDSRAVLCRNGQVCFSTQDKKPCNPVEKERIQNAG 183
QY 242 GFVANNLSGQPHVNGRLAMTRISIGDLK-----TSGVIA-EPETKRIKLHADDSEFL 293
DB 184 G-----SVMIQKRVNGSLAVSRALGDFYKCVHGKQTEQLVSPPEVYEI-VRAEEDEFV 237
QY 294 VLTDTGINFMVNSQIEICDFVQ-----CHDPNEAAHAYTEQAIQYGTEDNSTAVVVPF 346
DB 238 VLACDGIWDMVNGNEELCDFVRSRLVETDLDLEKVCNEVVDTCLYKGRDNMSVILVCF 294

RESULT 12
US-08-935-855-7
; Sequence 7, Application US/08935855
; Patent No. 6066485
; GENERAL INFORMATION:
; APPLICANT: Guthridge, Mark
; APPLICANT: Basilio, Claudio
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/935,855
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:

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; ORGANISM: Mus musculus
US-08-935-855-7

Query Match      15.4%; Score 300; DB 3; Length 309;
Best Local Similarity 31.3%; Pred. No. 1.7e-22;
Matches 93; Conservative 47; Mismatches 109; Indels 48; Gaps 11;

QY 88 PKISLENV-----GCASOIGKRKENEDR-----FDFQAQTDEVLVFAVYDGHGGPAA 134
DB 8 PKTEKNAHAGNGLRYGLSSMQGWRVEMEDAHTAVVGIPIHGLDWNWSFFAVYDGHAGSRV 67
QY 135 ADFCHTHM-----EKCIMDLPLKKNLETLTLAFLEIDKAFSSHARLSADA 181
DB 68 ANYCSTHLEHTTNEEDFRAAKSGSALESVSNKNGIRTGFLKIDEMRNFSDLRNG- 125
QY 182 TLTSTGTTATVALLRDGIELVVASVDSRAILCRKGKPKMLTIDHTPERKDEKERIKCG 241
DB 126 -MDRSGSTA-VGVMVSPTHMYFINCDSRAVLRCNGQVCFSTQDHKPCNPVEKERIQAG 183
QY 242 GFVAWNSLQPHVNGELAMTRISIGDLDLK-----TSGVIA-EPETKRIKLHHADDSFL 293
DB 184 G-----SVMTQRVNGSLAVSRALGDYDKVCGKGPTEQLVSPPEVYEI-VRAEEDBFV 237
QY 294 VLTTDGINFMVNSQEICDFVNC-----CHDPNEAAHATVTEQAIQVGTEDNSTAVVVPF 346
DB 238 VLACDGIWDMVMSNEELCEPVKSRLEVSDDLNVNVCNWWVDTCLHKGRDNMSIVLVCF 294

RESULT 13
US-08-873-093-1
; Sequence 1, Application US/08873093
; Patent No. 5853997
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,093
; FILING DATE: Filed Herewith
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0319 US
; TELEPHONE: 415-845-4166
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THPIPLB01

; CLONE: 13177
US-08-873-093-1

Query Match      14.5%; Score 282.5; DB 2; Length 478;
Best Local Similarity 29.2%; Pred. No. 2.1e-20;
Matches 92; Conservative 53; Mismatches 117; Indels 53; Gaps 11;

QY 88 PKISLENV-----GCASOIGKRKENEDR-----FDFQAQTDEVLVFAVYDGHGGPAA 134
DB 8 PKTEKNAHAGNGLRYGLSSMQGWRVEMEDAHTAVVGIPIHGLDWNWSFFAVYDGHAGSRV 67
QY 135 ADFCHTHM-----EKCIMDLPLKKNLETLTLAFLEIDKAFSSHARLSADA 181
DB 68 ANYCSTHLEHTTNEEDFRAAKSGSALESVSNKNGIRTGFLKIDEMRNFSDLRNG- 126
QY 182 TLTSTGTTATVALLRDGIELVVASVDSRAILCRKGKPKMLTIDHTPERKDEKERIKCG 241
DB 127 -MDRSGSTA-VGVMVSPTHMYFINCDSRAVLRCNGQVCFSTQDHKPCNPVEKERIQAG 184
QY 242 GFVAWNSLQPHVNGELAMTRISIGDLDLK-----TSGVIA-EPETKRIKLHHADDSFL 293
DB 185 G-----SVMTQRVNGSLAVSRALGDYDKVCGKGPTEQLVSPPEVYEI-LRAEEDFEI 238
QY 294 VLTTDGINFMVNSQEICDFVNC-----CHDPNEAAHATVTEQAIQVGTEDNSTAVVVPF 349
DB 239 ILACDGIWDMVMSNEELCEPVKSRLEVSDDLNVNVCNWWVDTCLHKGRDNMSIVLVCF 298
QY 350 GKY-----KNSEIN 358
DB 299 PKVSDAVKKDSELD 313

RESULT 14
US-08-873-093-4
; Sequence 4, Application US/08873093
; Patent No. 5853997
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,093
; FILING DATE: Filed Herewith
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0319 US
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
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STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 1452526
 US-08-873-093-4

Query Match 14.5%; Score 282.5; DB 2; Length 478;
 Best Local Similarity 29.2%; Pred. No. 2.1e-20;
 Matches 92; Conservative 53; Mismatches 117; Indels 53; Gaps 11;

QY 88 PKISLENV-----GCASQIGKRKENEDR-----FDFALQTDDEVLYFAVYDGHGPPAA 134
 DB 8 PKTEKHNAHGAGNGLRYGLSSMQGWRVEMEDAHAVVGIPIHGLEDSFFFAVYDGHAGSRV 67
 QY 135 ADFCHTMEKCIDM-----LLPKKLETLTLTFLAFLIDKAFSSSHARLSADA 181
 DB 68 ANYCSTHLEHITTNEEDFRAAGKSGSALELSVENVKNGIRGTGFLKIDEXYMRNFSDLRNG- 126
 QY 182 TLLTSGTTATVALLRDGIELVAVSGDSRAILCRKPKMKLTIDHTPERKDEKERIKKCG 241
 DB 127 -MDRSGSTA-VGMWISPKHIYFINGDSRAVLRYNGQVCFSTQDHKPCNPREKERIQNAG 184
 QY 242 GFVAMNSLGQPHVNGRLAMTRISIGDLK-----TSGVIA-EPETKRIKLHHADDSFL 293
 DB 185 G-----SVMIQRVNGSLAVSRALGDYKCVGKGPTQLVSPPEVYEI-LRAEDEFI 238
 QY 294 VLTDDGINFMVNSOEICDFVQ-----CHDPNEAAHAYTEQAICYGTEDNSTAVVVPFGAW 349
 DB 239 ILACDGIWVMSNEELCEYVKSRLVSDLENCVNVVDTCLHKGSRDNNMSIVLVCFNSA 298
 QY 350 GKY-----KNSEIN 358
 DB 299 PKVSDEAVKDSELD 313

RESULT 15
 US-09-206-646-1
 ; Sequence 1, Application US/09206646
 ; Patent No. 6436637
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Goli, Surya K.
 ; APPLICANT: Lal, Preeti G.
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Zhang, Hong
 ; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
 ; FILE REFERENCE: PF-0319-1 DIV
 ; CURRENT APPLICATION NUMBER: US/09/206,646
 ; CURRENT FILING DATE: 2001-12-07
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 1
 ; LENGTH: 479
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; OTHER INFORMATION: Incyte ID No. 6436637 013177CDI
 US-09-206-646-1

Query Match 14.5%; Score 282.5; DB 4; Length 479;
 Best Local Similarity 29.2%; Pred. No. 2.1e-20;
 Matches 92; Conservative 53; Mismatches 117; Indels 53; Gaps 11;
 QY 88 PKISLENV-----GCASQIGKRKENEDR-----FDFALQTDDEVLYFAVYDGHGPPAA 134
 DB 8 PKTEKHNAHGAGNGLRYGLSSMQGWRVEMEDAHAVVGIPIHGLEDSFFFAVYDGHAGSRV 67
 QY 135 ADFCHTMEKCIDM-----LLPKKLETLTLTFLAFLIDKAFSSSHARLSADA 181
 DB 68 ANYCSTHLEHITTNEEDFRAAGKSGSALELSVENVKNGIRGTGFLKIDEXYMRNFSDLRNG- 126

QY 182 TLLTSGTTATVALLRDGIELVAVSGDSRAILCRKPKMKLTIDHTPERKDEKERIKKCG 241
 DB 127 -MDRSGSTA-VGMWISPKHIYFINGDSRAVLRYNGQVCFSTQDHKPCNPREKERIQNAG 184
 QY 242 GFVAMNSLGQPHVNGRLAMTRISIGDLK-----TSGVIA-EPETKRIKLHHADDSFL 293
 DB 185 G-----SVMIQRVNGSLAVSRALGDYKCVGKGPTQLVSPPEVYEI-LRAEDEFI 238
 QY 294 VLTDDGINFMVNSOEICDFVQ-----CHDPNEAAHAYTEQAICYGTEDNSTAVVVPFGAW 349
 DB 239 ILACDGIWVMSNEELCEYVKSRLVSDLENCVNVVDTCLHKGSRDNNMSIVLVCFNSA 298
 QY 350 GKY-----KNSEIN 358
 DB 299 PKVSDEAVKDSELD 313

Search completed: October 12, 2004, 06:00:46
 Job time : 108 secs

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OM protein - protein search, using sw model

Run on: October 12, 2004, 05:55:18 ; Search time 98 Seconds
(without alignments)
1197.681 Million cell updates/sec

Title: US-10-716-488-2

Perfect score: 1951

Sequence: 1 MSTAALITLVRSQGNQVRRR.....KNSSEINFSSRSFSSGSGWA 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1951	100.0	372	4 Q8N3J5	Q8N3J5 homo sapien
2	1930	99.9	372	4 Q96NT4	Q96NT4 homo sapien
3	1945	99.7	372	4 Q8IUT7	Q8IUT7 homo sapien
4	1777	91.1	372	11 Q8BXN7	Q8BXN7 mus musculu
5	951.5	48.8	233	4 Q8IXG7	Q8IXG7 homo sapien
6	950	48.7	182	4 Q8ND70	Q8ND70 homo sapien
7	369	18.9	354	10 Q8LAY8	Q8LAY8 arabidopsis
8	360	18.5	348	10 Q8LEW5	Q8LEW5 arabidopsis
9	357	18.3	383	10 Q8M1P8	Q8M1P8 arabidopsis
10	352	18.0	282	10 Q7XR05	Q7XR05 oryza sativ
11	350.5	18.0	303	11 Q810HO	Q810HO mus musculu
12	350.5	18.0	360	11 Q8C021	Q8C021 mus musculu
13	350.5	18.0	360	11 Q8BHNO	Q8BHNO mus musculu
14	348	17.8	319	10 Q8S8Z0	Q8S8Z0 mesembryant
15	346.5	17.8	388	10 Q8H610	Q8H610 oryza sativ
16	344.5	17.7	392	10 Q9SLAI	Q9SLAI arabidopsis

17	344	17.6	311	10 Q8RXV3	Q8RXV3 arabidopsis
18	344	17.6	420	10 Q8VZD9	Q8VZD9 arabidopsis
19	342	17.5	394	10 Q84QD6	Q84QD6 nicotiana t
20	342	17.5	420	10 Q94AT1	Q94AT1 arabidopsis
21	340.5	17.5	380	10 Q9FYN7	Q9FYN7 oryza sativ
22	337.5	17.3	381	10 Q24078	Q24078 medicago sa
23	335	17.2	243	10 Q8G3P1	Q8G3P1 oryza sativ
24	334.5	17.1	362	10 Q92PL9	Q92PL9 lotus japon
25	334.5	17.1	380	10 Q8S8Z1	Q8S8Z1 mesembryant
26	333.5	17.1	371	10 Q8VZN9	Q8VZN9 arabidopsis
27	332.5	17.0	359	10 Q82469	Q82469 mesembryant
28	332	17.0	283	10 Q81714	Q81714 arabidopsis
29	332	17.0	467	10 Q81J68	Q81J68 oryza sativ
30	328	16.8	362	10 Q9ZW21	Q9ZW21 arabidopsis
31	326	16.7	307	10 Q9FCM3	Q9FCM3 arabidopsis
32	326	16.7	464	10 Q9FXE4	Q9FXE4 arabidopsis
33	324.5	16.6	511	10 Q8GWS8	Q8GWS8 arabidopsis
34	322.5	16.5	239	10 Q64583	Q64583 arabidopsis
35	322.5	16.5	528	10 Q93YS2	Q93YS2 arabidopsis
36	322.5	16.5	816	10 Q9M1V6	Q9M1V6 arabidopsis
37	322	16.5	283	10 Q94AE3	Q94AE3 arabidopsis
38	322	16.5	396	10 Q9LP12	Q9LP12 arabidopsis
39	322	16.5	511	10 Q9CAJ0	Q9CAJ0 arabidopsis
40	322	16.5	511	10 Q81709	Q81709 arabidopsis
41	321	16.5	271	10 Q9SM39	Q9SM39 sporobolus
42	320	16.4	355	10 Q81716	Q81716 arabidopsis
43	319.5	16.4	317	10 Q7XPM4	Q7XPM4 oryza sativ
44	319.5	16.4	389	10 Q81773	Q81773 arabidopsis
45	319.5	16.4	465	11 Q99ND8	Q99ND8 ratrus norv

ALIGNMENTS

RESULT 1

Q8N3J5 PRELIMINARY; PRT; 372 AA.

AC Q8N3J5; Q8N3J5; (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.

GN DKFZP761G058.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Amalgam.

RA Koshner K., Beyer A., Mewes H.W., Weil B., Wiemann S.;

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

EMBL; AL834271; CAD38946.1; -

DR GO; GO:0008287; C:Protein serine/threonine phosphatase complex; IEA.

DR GO; GO:0003824; F:Catalytic activity; IEA.

DR GO; GO:0004722; P:Protein serine/threonine phosphatase activity; IEA.

DR GO; GO:0006470; P:Protein amino acid dephosphorylation; IEA.

DR InterPro; IPR000222; PP2C.

DR InterPro; IPR001932; PP2C-like.

DR Pfam; PF00481; PP2C; 1.

DR SMART; SMC0332; PP2C; 1.

DR SMART; SMC0331; PP2C SIG; 1.

DR PROSITE; PS01032; PP2C; 1.

KW Hypothetical protein.

SK SEQUENCE 372 AA; 49997 MW; 9DD37EECEAD3313 CRC64;

Query Match 100.0%; Score 1951; DB 4; Length 372;

Best Local Similarity 100.0%; Pred. No. 7.5e-160;

Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTAALITLVRSQGNQVRRVLLSSRLLODRVTPCHSSTSEPRCSRPDPGSGSPAT 60

Db 1 MSTAALITLVRSQGNQVRRVLLSSRLLODRVTPCHSSTSEPRCSRPDPGSGSPAT 60

QY 61 WDNFGIWNDRIDEPIILLPPSIKYGKPIPKISLENVGCASQIGRKENEDRFDFAQLTDEV 120
 Db 61 WDNFGIWNDRIDEPIILLPPSIKYGKPIPKISLENVGCASQIGRKENEDRFDFAQLTDEV 120
 QY 121 LYFAYVDGHHGPPAAADFCHTHMEKCIIMDLLPKENKLETLTLTFLAFLEIDKAFSSHARLSAD 180
 Db 121 LYFAYVDGHHGPPAAADFCHTHMEKCIIMDLLPKENKLETLTLTFLAFLEIDKAFSSHARLSAD 180
 QY 181 ATLLTSGTTATVALLRGGIELVWASVGDRAILCRKKGPKMLTIDHTPERKDEKERIKKC 240
 Db 181 ATLLTSGTTATVALLRGGIELVWASVGDRAILCRKKGPKMLTIDHTPERKDEKERIKKC 240
 QY 241 GGFVAMNSLGOPHVNGLAMTRISIGDLTKTSGVIAEPETKRIKLHADDSEFLVLTDDGI 300
 Db 241 GGFVAMNSLGOPHVNGLAMTRISIGDLTKTSGVIAEPETKRIKLHADDSEFLVLTDDGI 300
 QY 301 NFMVNSQICDFVNOCHDPNEAAHVAITEQAIQYGTEDNSTAVVVPFGAWGKYKXSEINFS 360
 Db 301 NFMVNSQICDFVNOCHDPNEAAHVAITEQAIQYGTEDNSTAVVVPFGAWGKYKXSEINFS 360
 QY 361 FSRSFASSGRWA 372
 Db 361 FSRSFASSGRWA 372

RESULT 2

Q96NT4 ID Q96NT4 PRELIMINARY; PRT; 372 AA.
 AC Q96NT4; 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Hypothetical protein FLJ30116.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Cerebellum;
 RA Nishi T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H.,
 RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
 RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
 RA Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
 RA Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,
 RA Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
 RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
 RT "NEDO human cDNA sequencing project."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
 DR EMBL; AK054678; BAB70790.1; -;
 DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0000287; F:magnesium ion binding; IEA.
 DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR000222; PP2C.
 DR InterPro; IPR001332; PP2C-like.
 DR Pfam; PF00481; PP2C; 1.
 DR SMART; SM00332; PP2Cc; 1.
 DR SMART; SM00331; PP2C SIG; 1.
 DR PROSITE; PS01032; PP2C; 1.
 KW Hypothetical protein; Hydrolase; Magnesium.
 SQ SEQUENCE 372 AA; 40983 MW; 7065B29DC79CB93B CRC64;

Query Match 99.9%; Score 1950; DB 4; Length 372;
 Best Local Similarity 99.7%; Pred. No. 9.2e-160;
 Matches 371; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNQVRRVLLSRLLQDDRRVTPTCHSSTSPRCRFPDGGSGSPAT 60
 Db 1 MSTAALITLVRSQGNQVRRVLLSRLLQDDRRVTPTCHSSTSPRCRFPDGGSGSPAT 60

QY 61 WDNFGIWNDRIDEPIILLPPSIKYGKPIPKISLENVGCASQIGRKENEDRFDFAQLTDEV 120
 Db 61 WDNFGIWNDRIDEPIILLPPSIKYGKPIPKISLENVGCASQIGRKENEDRFDFAQLTDEV 120
 QY 121 LYFAYVDGHHGPPAAADFCHTHMEKCIIMDLLPKENKLETLTLTFLAFLEIDKAFSSHARLSAD 180
 Db 121 LYFAYVDGHHGPPAAADFCHTHMEKCIIMDLLPKENKLETLTLTFLAFLEIDKAFSSHARLSAD 180
 QY 181 ATLLTSGTTATVALLRGGIELVWASVGDRAILCRKKGPKMLTIDHTPERKDEKERIKKC 240
 Db 181 ATLLTSGTTATVALLRGGIELVWASVGDRAILCRKKGPKMLTIDHTPERKDEKERIKKC 240
 QY 241 GGFVAMNSLGOPHVNGLAMTRISIGDLTKTSGVIAEPETKRIKLHADDSEFLVLTDDGI 300
 Db 241 GGFVAMNSLGOPHVNGLAMTRISIGDLTKTSGVIAEPETKRIKLHADDSEFLVLTDDGI 300
 QY 301 NFMVNSQICDFVNOCHDPNEAAHVAITEQAIQYGTEDNSTAVVVPFGAWGKYKXSEINFS 360
 Db 301 NFMVNSQICDFVNOCHDPNEAAHVAITEQAIQYGTEDNSTAVVVPFGAWGKYKXSEINFS 360
 QY 361 FSRSFASSGRWA 372
 Db 361 FSRSFASSGRWA 372

RESULT 3

Q8IUZ7 ID Q8IUZ7 PRELIMINARY; PRT; 372 AA.
 AC Q8IUZ7; 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Pancreas;
 RA Strausberg R.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC037552; AAH37552.1; -;
 DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR000222; PP2C.
 DR InterPro; IPR001332; PP2C-like.
 DR Pfam; PF00481; PP2C; 1.
 DR SMART; SM00332; PP2Cc; 1.
 DR SMART; SM00331; PP2C SIG; 1.
 DR PROSITE; PS01032; PP2C; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 372 AA; 41011 MW; 29927CBB2DD32A2 CRC64;

Query Match 99.7%; Score 1945; DB 4; Length 372;
 Best Local Similarity 99.7%; Pred. No. 2.5e-159;
 Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNQVRRVLLSRLLQDDRRVTPTCHSSTSPRCRFPDGGSGSPAT 60
 Db 1 MSTAALITLVRSQGNQVRRVLLSRLLQDDRRVTPTCHSSTSPRCRFPDGGSGSPAT 60
 QY 61 WDNFGIWNDRIDEPIILLPPSIKYGKPIPKISLENVGCASQIGRKENEDRFDFAQLTDEV 120
 Db 61 WDNFGIWNDRIDEPIILLPPSIKYGKPIPKISLENVGCASQIGRKENEDRFDFAQLTDEV 120
 QY 121 LYFAYVDGHHGPPAAADFCHTHMEKCIIMDLLPKENKLETLTLTFLAFLEIDKAFSSHARLSAD 180
 Db 121 LYFAYVDGHHGPPAAADFCHTHMEKCIIMDLLPKENKLETLTLTFLAFLEIDKAFSSHARLSAD 180

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QY 181 ATLLTSGTTATVALLRDGIELVVASVGSRAILCRKKGPKMLTIDHTPERKDEKERIKK 240
Db 181 ATLLTSGTTATVALLRDGIELVVASVGSRAILCRKKGPKMLTIDHTPERKDEKERIKK 240
QY 241 GGFVAVNSLIGQPHVNGRLAMTRISIGDLDKTSGVIAEPETTKRIKLHHADDSFLVLTDDGI 300
Db 241 GGFVAVNSLIGQPHVNGRLAMTRISIGDLDKTSGVIAEPETTKRIKLHHADDSFLVLTDDGI 300
QY 301 NFWNSQICDFVNOCHDPNEAAHVAITEQAIQYGTEDNSTAVVVPFGAWGKYKNSINF 360
Db 301 NFWNSQICDFVNOCHDPNEAAHVAITEQAIQYGTEDNSTAVVVPFGAWGKYKNSINF 360
QY 361 FSRSPASSGRWA 372
Db 361 FSRSPASSGRWA 372

RESULT 4
Q8BXN7 PRELIMINARY; PRT; 372 AA.
AC Q8BXN7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein serine/threonine phosphatase 2C structure
DE containing protein.
GN A930026L03RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Retina;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK044610; BAC32001.1; -.
DR PIR; PT0546; PT0698.
DR MGI; MGI:2442111; A930036L03RIK.
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2CC; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hypothetical protein.
SQ SEQUENCE 372 AA; 40918 MW; 3749BBB94F211E7A CRC64;

Query Match 91.1%; Score 1777; DB 11; Length 372;
Best Local Similarity 90.3%; Pred. No. 7.8e-145;
Matches 336; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60
Db 1 MLSAAITLVRSQGNQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60
QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGRKENEDRFPDGLTDEV 120
Db 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASLIGRKENEDRFPDGLTDEV 120
QY 121 LYFAVYDGHGGPAAADFCPTHMEKCIIMDLLPKENKLETLTLTFLAFLDKAFSSHARLSAD 180
Db 121 LYFAVYDGHGGPAAADFCPTHMEKCIIMDLLPKENKLETLTLTFLAFLDKAFASYAHLASD 180
QY 181 ATLLTSGTTATVALLRDGIELVVASVGSRAILCRKKGPKMLTIDHTPERKDEKERIKK 240
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Db 181 ASLLTSGTTATVALLRDGIELVVASVGSRAILCRKKGPKMLTIDHTPERKDEKERIKK 240
QY 241 GGFVAVNSLIGQPHVNGRLAMTRISIGDLDKTSGVIAEPETTKRIKLHHADDSFLVLTDDGI 300
Db 241 GGFVAVNSLIGQPHVNGRLAMTRISIGDLDKTSGVIAEPETTKRIKLHHADDSFLVLTDDGI 300
QY 301 NFWNSQICDFVNOCHDPNEAAHVAITEQAIQYGTEDNSTAVVVPFGAWGKYKNSINF 360
Db 301 NFWNSQICDFVNOCHDPNEAAHVAITEQAIQYGTEDNSTAVVVPFGAWGKYKNSINF 360
QY 361 FSRSPASSGRWA 372
Db 361 FSRSPASSGRWA 372

RESULT 5
Q8IXG7 PRELIMINARY; PRT; 233 AA.
AC Q8IXG7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE UG0882E07.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Mac Y., Xie Y.;
RT "Isolation of full-length cDNA clones from human fetal brain cDNA
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF351614; AAN76514.1; -.
DR PIR; PT0240.
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
SQ SEQUENCE 233 AA; 25692 MW; EB90A7B3BC1BDD08 CRC64;

Query Match 48.8%; Score 951.5; DB 4; Length 233;
Best Local Similarity 86.6%; Pred. No. 6.9e-74;
Matches 187; Conservative 5; Mismatches 17; Indels 7; Gaps 1;

QY 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60
Db 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60
QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGRKENEDRFPDGLTDEV 120
Db 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGRKENEDRFPDGLTDEV 120
QY 121 LYFAVYDGHGGPAAADFCPTHMEKCIIMDLLPKENKLETLTLTFLAFLDKAFSSHARLSAD 180
Db 121 LYFAVYDGHGGPAAADFCPTHMEKCIIMDLLPKENKLETLTLTFLAFLDKAFSSHARLSAD 180
QY 181 ATLLTSGT-----TATVALLRDGIELVVASVGS 209
Db 181 ENCWSAALDLEPVDVTTCGSVEREICLLISQVKES 216

RESULT 6
Q8ND70 PRELIMINARY; PRT; 182 AA.
AC Q8ND70;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN DKFZP667B084.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP TISSUE=Lymph Node.
 RC SEQUENCE FROM N.A.
 RA Ansoerger W., Winkler U., Mewes H.W., Weil B., Wiemann S.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL834167; CAD38869.1; -
 DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0004722; P:protein serine/threonine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR000222; PP2C.
 DR InterPro; IPR001932; PP2C-like.
 DR Pfam; PF00481; PP2C; 1.
 DR PROSITE; PS01032; PP2C; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 182 AA; 20239 MW; 0D2523DB99A810BB CRC64;

 Query Match 48.7%; Score 950; DB 4; Length 182;
 Best Local Similarity 100.0%; Pred. No. 6.5e-74;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVTPCHSSTSEPRCSRFPDGGSGSPAT 60
 DB 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVTPCHSSTSEPRCSRFPDGGSGSPAT 60

 QY 61 WDNFGIWNDRIDEPIILPPSIKYGKPKISLENVGCASQIGRKENEDRFPDPAQLTDEV 120
 DB 61 WDNFGIWNDRIDEPIILPPSIKYGKPKISLENVGCASQIGRKENEDRFPDPAQLTDEV 120

 QY 121 LYFVAVDGHGGPAAADFCHTHMEKINDLLPKENLTLLTFLAFLEIDKAFSSHARLSAD 180
 DB 121 LYFVAVDGHGGPAAADFCHTHMEKINDLLPKENLTLLTFLAFLEIDKAFSSHARLSAD 180

 RESULT 7
 Q8LAY8 PRELIMINARY; PRT; 354 AA.
 ID Q8LAY8
 AC Q8LAY8
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE Protein phosphatase 2C-like protein (Hypothetical protein).
 GN AT5G10740/T30N20 10 OR AT5G10740.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 RT annotation.";
 RL Genome Biol. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;
 RT "Full-length cDNA from Arabidopsis thaliana";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
 RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,

RA Hayashizaki Y., Shinozaki K.;
 RT "Arabidopsis thaliana full-length cDNA";
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
 RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
 RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
 RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
 RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
 RA Schwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RT "Arabidopsis Open Reading Frame (ORF) Clones";
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY087522; AAM65064.1; -
 DR EMBL; AK117549; BAC42210.1; -
 DR EMBL; BT005431; AAC63851.1; -
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO; GO:0006287; C:protein serine/threonine phosphatase complex; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0004722; P:protein serine/threonine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001933; Mitoch_carrier.
 DR InterPro; IPR000222; PP2C.
 DR InterPro; IPR001932; PP2C-like.
 DR Pfam; PF00481; PP2C; 1.
 DR SMART; SM00332; PP2C; 1.
 DR PROSITE; PS00331; PP2C_SIG; 1.
 DR PROSITE; PS00215; MITOCH_CARRIER; 1.
 DR PROSITE; PS01032; PP2C; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 354 AA; 38036 MW; 87DA535B561C9D68 CRC64;

 Query Match 18.9%; Score 369; DB 10; Length 354;
 Best Local Similarity 36.1%; Pred. No. 2.3e-23;
 Matches 101; Conservative 56; Mismatches 93; Indels 30; Gaps 11;

 QY 96 GCASQIGRKKNEDRFPD--FAQLTDEVL-YFVAVDGHGGPAAADFCHTHMEKINDLLPK 152
 DB 35 GYASSAGKRSMEDFFETRIDGNGEIVGLFGVDFGHGGAAAEYVRHL---FSNLITH 91

 QY 153 EK--NLETTLLTFLAFLEID---KAFSSHARLSADATLLTSGTTATVALLRDGIELVVAS 205
 DB 92 PKFISDTKSAITDAYNHTDSELLKSENHR-----DAGSTASTAIL-VGDRLVAN 142

 QY 206 VGDRAILCRKGPKMKLTIDHTPERKOEKERIKCGGFFVAVNSLGQPHVNGRLAMTRSIG 265
 DB 143 VGDGRAVISRGKKAIAVSRDKPKQSDERERENAGGFVVM--AGTWRVGGVLAVSRAFG 200

 QY 266 DLDLKTSGVIAEPETKRIKLHADD--FLVLTDTGDNFVNSOEICDFVNOCHDRNEAA 323
 DB 201 DRLKQ-QVAVADPEIQEKI---DITLFLILASDGLWDFVSNFAAVAMVKEVDEPDSA 256

 QY 324 HAVTEQAIQYCTEDNSTAVVFPFGANGKYNKSEINFPSR 363
 DB 257 KKLVGKALKRGSAADNTICVVVRFLEKKKSSSSSHSSSSSK 296

 RESULT 8
 Q9LEW5 PRELIMINARY; PRT; 348 AA.
 ID Q9LEW5
 AC Q9LEW5
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE Protein phosphatase 2C-like protein.
 GN T30N20_10.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.


```

Db 92 NNAVYSIQGRDHMEDRFEVLTLANKTHPSI - FGIPDHGGGTAAEYVKSRLEALQKH 150
Qy 150 L-----PKEKNI---ETLLTLAFLEIDKAFSSHARLSADATLLTSGTTATVALLRDGIEL 201
Db 151 LDYKDKKNSVLTQTILEEQIISIDREMLEKLTVDYD----EAGTCLIALLSDK-DL 205
Qy 202 VVASVGDRAILCRK-GKPMKLTIDHTPERKDEKERIKKCGGFVAVNSLGGQPHVNGRLAM 260
Db 206 TVANVGDSRGVLCXGDNALPLSHDKPYQLKERKRIKRAAGGF-SFN--GSRVVOGILAM 263
Qy 261 TRSIGDLDLKT-SGVIAEPETKRIKLHHADDSFLVLTDTGGINFMVNSQEIICDFVNO-CHD 318
Db 264 SRSLGDYPLKNVWIPDPDILTFLDKLQPEFMILASDGLWDAFNSBAVRFIKERLDE 323
Qy 319 PNEAAHVAITEQAIOYGTEDNSTAVVVPFGAMKYKNS 355
Db 324 PHFGAKSIVLQSFYRGCPDNITVMVV-----KFRNS 354

RESULT 13
Q8BHN0 PRELIMINARY; PRT; 360 AA.
AC Q8BHN0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CDNA FLJ303553 FIS.
GN AI481720.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Brain, and Cerebellum;
RC MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK035912; BAC29241.1; -.
DR EMBL; AK045724; BAC32472.1; -.
DR MGD; MGI:2139740; AI481720.
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0003824; F:Catalytic activity; IEA.
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000222; PP2C.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2Cc; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
SQ SEQUENCE 360 AA; 41049 MW; 026CAC7687E5EA1E CRC64;

Query Match 18.0%; Score 350.5; DB 11; Length 360;
Best Local Similarity 34.3%; Pred. No. 9.5e-22;
Matches 95; Conservative 52; Mismatches 101; Indels 29; Gaps 11;

Qy 94 NVGCSAQIGKRKENEDRF----DFQLTDEVLYFVYDGHGGPAAADFCHTHMEKIMDL 149
Db 92 NNAVYSIQGRDHMEDRFEVLTLANKTHPSI - FGIPDHGGGTAAEYVKSRLEALQKH 150
Qy 150 L-----PKEKNI---ETLLTLAFLEIDKAFSSHARLSADATLLTSGTTATVALLRDGIEL 201
Db 151 LDYKDKKNSVLTQTILEEQIISIDREMLEKLTVDYD----EAGTCLIALLSDK-DL 205
Qy 202 VVASVGDRAILCRK-GKPMKLTIDHTPERKDEKERIKKCGGFVAVNSLGGQPHVNGRLAM 260
Db 206 TVANVGDSRGVLCXGDNALPLSHDKPYQLKERKRIKRAAGGF-SFN--GSRVVOGILAM 263
Qy 261 TRSIGDLDLKT-SGVIAEPETKRIKLHHADDSFLVLTDTGGINFMVNSQEIICDFVNO-CHD 318

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Db 264 SRSLGDYPLKNVWIPDPDILTFLDKLQPEFMILASDGLWDAFNSBAVRFIKERLDE 323
Qy 319 PNEAAHVAITEQAIOYGTEDNSTAVVVPFGAMKYKNS 355
Db 324 PHFGAKSIVLQSFYRGCPDNITVMVV-----KFRNS 354

RESULT 14
Q8S8Z0 PRELIMINARY; PRT; 319 AA.
AC Q8S8Z0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Protein phosphatase 2C.
GN MPC9.
OS Mesembryanthemum crystallinum (Common ice plant).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Alzooaceae; Mesembryanthemum.
OX NCBI_TaxID=3544;
RN [1]_
SEQUENCE FROM N.A.
RP Miyazaki S., Izumi S., Fukuhara T., Bohnert H.J.;
RA "Plant Protein Phosphatases 2C ? A large protein family serving
RT complex functions.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
DR EMBL; AB083482; BAB8944.1; -.
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2Cc; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydrolase; Magnesium.
SQ SEQUENCE 319 AA; 34477 MW; 0BD228603E34CFB0 CRC64;

Query Match 17.8%; Score 348; DB 10; Length 319;
Best Local Similarity 36.6%; Pred. No. 1.3e-21;
Matches 97; Conservative 45; Mismatches 89; Indels 34; Gaps 10;

Qy 96 GCASQIGKRKENED----RFDAQLTDEVLYFVYDGHGGPAAADFCHTHMEKIMDL 151
Db 35 GYASSPGKSSMEDFYETRIDGVE-GEVVGIFGVDFDGHGGAAYVKQL---FSLIK 90
Qy 152 KEKNLETLTLTALFLIDKAFSSHARLSADATLLTS-----GTTATVALLRDGIELV 203
Db 91 HPK-----FISDTKSAIAEAYTHDSEFLKSENTQNRDAGSTASTAIL-VGDRLLV 140
Qy 204 ASVGDSRAILCRKGPMLKLTIDHTPERKDEKERIKKCGGFVAVNSLGGQPHVNGRLAMTRS 263
Db 141 ANVGDSRAVICRGGEALAVSRDKPKQSDERQIEDAGGFVWV--AGTWRVGGVLAWSRA 198
Qy 264 IGDLDLTKTSVIAEPETKRIKLHHADDS--FLVLTDTGGINFMVNSQEIICDFVNOCHD 321
Db 199 FGDKLLK-QYVADPE---IQEEVVDSSLEFLILASDGLWDAFNSBAVRFIKERLDE 254
Qy 322 AAHVAITEQAIOYGTEDNSTAVVVPFG 346
Db 255 AAKLMQEAQYRGSAADNITCVVVR 279

RESULT 15
Q8H610 PRELIMINARY; PRT; 388 AA.
AC Q8H610;

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01-MAR-2003 (TRENBLrel. 23, Created)
01-MAR-2003 (TRENBLrel. 23, Last sequence update)
01-OCT-2003 (TRENBLrel. 25, Last annotation update)
Putative DNA-binding protein phosphatase 2C.
OSJNBA0035103.17.
Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriactoidae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, BAC
clone:OSJNBA0035103.17";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003019; BAC22243.1; -.
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR002222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
KW DNA-binding.
KW DNA-binding.
SQ SEQUENCE 388 AA; 42397 MW; B614776245AF9D77 CRC64;
Query Match 17.8%; Score 346.5; DB 10; Length 388;
Best Local Similarity 32.6%; Pred. No. 2.3e-21;
Matches 94; Conservative 55; Mismatches 98; Indels 41; Gaps 10;
Qy 82 KYGKPIPKISLENVGCSAQIGKRENE-----RDFPAQLTDEVLYFAVYDGHG 130
Db 84 KSGNFVFN-----RSGDWSDIGGRQYMEDTHVCITDLAKNFGYQSVNDNEAISFYGVFDGHG 140
Qy 131 GPAADFCHTHMEKICMDLLPKENLTLLTAFLEIDKAFSSHARLSADATLLTSGTTA 190
Db 141 GKDAHFVRDNLPLIIVEDADFFLELEKVVRSFVHADNQFAK-----TTLSSGTTA 192
Qy 191 TVALLRGIELVVASGDSRAILCRKPKMKLTIDHTPERKDEKERIKCGGFVANNSLG 250
Db 193 LTAMI-FGRTILLIANAGDCRAVLSCGTAIEMSVDRPCSLSEKLRVESLGGYV-----D 246
Qy 251 QPHVNGRLAMTRSIGDLDL---KTSG---VIAEPETKRIKLHADDSDLVLTDTGINF 302
Db 247 DGYLNGLLGVTRAUGDHLGMEKAGNPGGFLSAEPELQMITL-TKDDFLIIGSDGIWD 305
Qy 303 MVNSQEICDF----VNOCHDPNEAAHVAVTQAIQYGTEDNSTAVVVPF 346
Db 306 VFSNQNVVDFARRLQEHNDVKSCREIVEEAKRGATDNLTAVLVSF 353

Search completed: October 12, 2004, 06:02:43
Job time : 105 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 12, 2004, 05:55:18 ; Search time 22 Seconds
(without alignments)
880.459 Million cell updates/sec

Title: US-10-716-488-2

Perfect score: 1951

Sequence: 1 MSTAALITLVRSGNQVRR.....KNSINFSTRSPASSGRWA 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	354.5	18.2	423	1 P2C2_ARATH	O04719 arabidopsis
2	338	17.3	434	1 P2C1_YEAST	P49597 arabidopsis
3	325	16.7	281	1 P2C1_YEAST	P35182 saccharomyc
4	321.5	16.5	347	1 P2C1_SCHPO	P40371 schizosacch
5	319.5	16.4	390	1 P2C8_RAT	P35815 rattus norv
6	310.5	15.9	383	1 P2C4_SCHPO	O14156 schizosacch
7	307.5	15.8	382	1 P2CA_BOVIN	O62829 bos taurus
8	307.5	15.8	382	1 P2CA_HUMAN	P35813 homo sapien
9	307.5	15.8	390	1 P2CB_MOUSE	P36993 mus musculu
10	306.5	15.7	382	1 P2CA_MOUSE	P49443 mus musculu
11	306.5	15.7	382	1 P2CA_RABIT	P35814 oryctolagus
12	306.5	15.7	382	1 P2CN_RAT	P20650 rattus norv
13	306.5	15.7	414	1 P2C3_SCHPO	Q09173 schizosacch
14	305	15.6	370	1 P2C2_SCHPO	Q09172 schizosacch
15	300.5	15.4	300	1 P2C2_PART	P49444 paramecium
16	297.5	15.2	387	1 P2CB_BOVIN	O62830 bos taurus
17	290.5	14.9	454	1 FEM2_HUMAN	P49593 homo sapien
18	282.5	14.5	479	1 P2CB_HUMAN	O75688 homo sapien
19	281	14.4	399	1 P2C4_ARATH	P49598 arabidopsis
20	279	14.3	406	1 P2C2_LEICH	P36992 leishmania
21	278	14.2	356	1 P2C2_CAEEL	P49596 caenorhabdi
22	264	13.5	450	1 FEM2_RAT	Q9wv77 rattus norv
23	264	13.5	468	1 P2C3_YEAST	P34221 saccharomyc
24	260	13.3	468	1 P2C3_YEAST	P34221 saccharomyc
25	228.5	11.7	542	1 P2CQ_MOUSE	O61074 mus musculu
26	226.5	11.6	491	1 P2C1_CAEEL	P49595 caenorhabdi
27	226	11.6	546	1 P2CG_HUMAN	O15355 homo sapien
28	223	11.4	543	1 P2CG_BOVIN	P79126 bos taurus
29	219	11.2	605	1 P2CD_HUMAN	O15297 homo sapien
30	218	11.2	598	1 P2CD_MOUSE	Q9qz67 mus musculu
31	216	11.1	388	1 P2C3_ARATH	P49599 arabidopsis
32	206.5	10.6	1839	1 CYAA_SACKL	P23466 saccharomyc
33	204	10.5	2026	1 CYAA_YEAST	P08678 saccharomyc

ALIGNMENTS

RESULT 1

ID	P2C2_ARATH	STANDARD;	PRT;	423 AA.
AC	O04719;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Protein phosphatase 2C AB12 (EC 3.1.3.16) (P2C2) (Abscisic acid-insensitive 2).			
GN	AB12 OR AT5G57050 OR MEM17.19.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.			
OX	NCBI_TaxID=3702;			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia, and cv. Landsberg erecta;			
RX	MEDLINE=97308526; PubMed=9165752;			
RA	Leung J., Merlot S., Giraudat J.;			
RT	"The Arabidopsis ABSCISIC ACID-INSENSITIVE2 (AB12) and AB11 genes encode homologous protein phosphatases 2C involved in abscisic acid signal transduction."			
RL	Plant Cell 9:759-771(1997).			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Landsberg erecta;			
RX	Rodriguez P.L., Grill E.;			
RA	Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
RX	MEDLINE=20181125; PubMed=10718197;			
RA	Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,			
RT	"Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty P1 and TAC clones."			
RL	DNA Res. 7:31-63(2000).			
CC	FUNCTION: Involved in abscisic acid (ABA) signaling pathway.			
CC	CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein + phosphate.			
CC	COFACTOR: Binds 2 magnesium or manganese ions (By similarity).			
CC	SIMILARITY: Belongs to the P2C2 family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch .			
CC	EMBL; Y08966; CAA70163.1; -			
DR	EMBL; Y08965; CAA70162.1; -			
DR	EMBL; Y11840; CAA72338.1; -			

34	202.5	10.4	393	1	P2C4_YEAST	P38089 saccharomyc
35	194.5	10.0	442	1	YCW9_YEAST	P25646 saccharomyc
36	192	9.8	449	1	FEM2_CAEEL	P49594 caenorhabdi
37	181.5	9.3	2145	1	CYAA_PODAN	Q01513 podospora a
38	175.5	9.0	2493	1	CYAA_USMA	P49606 ustilago ma
39	170.5	8.7	504	1	TYAA_HUMAN	Q15750 homo sapien
40	169	8.7	2300	1	CYAA_NEUCR	Q01631 neurospora
41	164.5	8.4	538	1	PDP1_BOVIN	P35816 bos taurus
42	159	8.1	581	1	KAPP_ARATH	P46014 arabidopsis
43	153.5	7.9	538	1	PDP1_RAT	O88483 rattus norv
44	150.5	7.7	529	1	PDP2_HUMAN	Q9P019 homo sapien
45	149.5	7.7	538	1	PDP1_HUMAN	Q9P011 homo sapien

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DR EMBL; AB024035; BAA7035.1; -.
DR HSSP; P35813; 1A60.
DR InterPro; IPR001932; P2C-like.
DR InterPro; IPR000222; P2C.
DR Pfam; PF00481; P2C; 1.
DR SMART; SMO0331; P2C SIG; 1.
DR SMART; SMO0332; P2C; 1.
DR PROSITE; PS01032; P2C; 1.
DR Hydrolase; Magnesium; Manganese; Multigene family; Calcium-binding.
FT CA BIND 70 81 EF-HAND (POTENTIAL)
SQ SEQUENCE 423 AA; 46306 MW; 67CAAC76DAS31A7I CRC64;

Query Match      18.2%; Score 354.5; DB 1; Length 423;
Best Local Similarity 30.6%; Pred. No. 3.7e-22;
Matches 99; Conservative 51; Mismatches 99; Indels 75; Gaps 12;

QY 96 GCASQIGRKENEDRFD-----FAQLTDEVL-----YFAYVDGCGPAAA 135
Db 114 GVSICGRPEWDSVSTIPFLQVSSSLDGRVTNGFNPHLSAHPFGYDGHGGSQA 173
QY 136 DFCHEKMEKICMDLLPKK-----NLETLTLAFLIEDIKAFSPSHARLSADATLL 184
Db 174 NYCRRMHLALTEIVKEKPEFCGDTWQEKWKALFNSFMRVDSSETETVAHPE----- 228
QY 185 TSGTATVALRDGIELVWASVGSRAILCRKKGPKMLTIDHTPERKDEKERIKCGG-F 243
Db 229 TVGSTVAVVFP-THIFVANGSDRAVLGRGTPLALSDVDHPRDRDEAARTEAAGKV 287
QY 244 VAMSLGPHVNGRLAMTRISGDLTKTSGVIAEPE---TKRKLHHADDSFLVLTTDGI 300
Db 288 IRWNG---ARVFGVLAMRSIGDRYLKPS-VIPDPVTSVRRVK-----EDDCILASDGL 339
QY 301 NFMVNSQICDFVQ-----CHDPN-----EAAHVVTEQAIQYG 334
Db 340 WDVNTNEVCDLARKILLHKKNAAGEALLPAEKTRGEGKDPAAWSAAYLSKMAIQK 399
QY 335 TEDNSTAVVFPFGAWGVKNSIN 358
Db 400 SKDNISVVVDLKGIRAFKSKSLN 423

RESULT 2
P2C1 ARATH STANDARD; PRT; 434 AA.
AC P48597; Q43717; Q94C87.
DT 01-FEB-1996 (Rel. 33, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE DE Protein phosphatase 2C AB11 (EC 3.1.3.16) (P2C) (Abscisic acid-
DE insensitive 1).
GN AB11 OR AT4G26080 OR P20B18.190.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OC NCBI_TaxID=3702;
[1]
RN RP SEQUENCE FROM N.A., AND VARIANT ASP-180.
RC STRAIN=cv. Landsberg erecta;
RX MEDLINE=94255767; PubMed=9197457;
RA Meyer K., Leube W.P., Grill E.;
RT "A protein phosphatase 2C involved in ABA signal transduction in
RT Arabidopsis thaliana."
RL Science 264:1452-1455(1994).
[2]
RN RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia; TISSUE=Leaf;
RX MEDLINE=95007759; PubMed=7923358;
RA Mindrinos M., Katagiri F., Yu G.L., Ausubel F.M.;
RT "The A. thaliana disease resistance gene RPS2 encodes a protein
RT containing a nucleotide-binding site and leucine-rich repeats."
RL Cell 78:1089-1099(1994).
[3]

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RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia; TISSUE=Leaf;
RX MEDLINE=94255766; PubMed=7910981;
RA Leung J., Bouvier-Durand M., Morris P.C., Guerrier D., Chefdor F.,
RA Giraudat J.;
RT "Arabidopsis ABA response gene ABI1: features of a calcium-modulated
RT protein phosphatase."
RL Science 264:1448-1452(1994).
[4]
RN RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198;
RA Pohl K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Mayer T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,
RA Harris B., Ansong W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA Reichert B., Portetelle D., Zimmermann W., Wedler M., Schmittheini T.,
RA Vos P., Hoheisel J., Zimmermann W., Boutry M., Bancroft I.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weitzenegger T., Bothe G., Ransperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren W., Dikse W.,
RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., van den Daele H.,
RA De Keyser A., Buysshaert C., Gielens J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Reckmann S.,
RA Borkova D., Bloeker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Neumann S., Argüioley A., Vitale D., Liguori R., Piravandi E.,
RA Massenet O., Quigley F., Clabaud G., Muendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Bagues M., Terol J., Torres A.,
RA Perez-Perez A., Furnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheer P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M.A., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana."
RL Nature 402:769-777(1999).
[5]
RN RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=22954850; PubMed=14593172;
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J., Cheuk R.F.,
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.L., Trapp M., Chang C.H., Lee J.M., Toiuni M.J.,
RA Chan M.T., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Anzari P.,
RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,

```

RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RT "Empirical analysis of transcriptional activity in the Arabidopsis
 RL genome.";
 CC -!- FUNCTION: Involved in abscisic acid (ABA) signaling pathway.
 CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
 CC -!- SIMILARITY: Belongs to the PP2C family.
 CC
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 DR EMBL; X78886; CAA55484.1; -;
 DR EMBL; U12856; CAA50237.1; -;
 DR EMBL; X77116; CAA54383.1; -;
 DR EMBL; AL049483; CAB39673.1; -;
 DR EMBL; AL161564; CAB79463.1; -;
 DR EMBL; AY035073; AAK59578.1; -;
 DR PIR; T04263; T04263.
 DR HSSP; P35813; IAGQ.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR001932; PP2C-like.
 DR InterPro; IPR000222; PP2C.
 DR Pfam; PF00481; PP2C; 1.
 DR SMART; SM00331; PP2C_SIG; 1.
 DR SMART; SM00332; PP2C; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS01032; PP2C; 1.
 DR KW Hydroxylase; Magnesium; Manganese; Multigene family; Calcium-binding.
 FT CA BIND 93 104 EF-HAND (POTENTIAL).
 FT DOMAIN 417 420 POLY-VAL.
 FT VARIANT 180 180 G -> D (WILTY PHENOTYPE AND ABA-
 FT INSENSITIVE SEED GERMINATION AND GROWTH).
 FT CONFLICT 24 24 G -> R (IN REF. 5).
 FT CONFLICT 105 105 I -> V (IN REF. 1).
 FT SEQUENCE 434 AA; 47505 MW; 4A4C54F04195F572 CRC64;
 SQ
 Query Match 17.3%; Score 338; DB 1; Length 434;
 Best Local Similarity 30.9%; Pred. No. 9.3e-21;
 Matches 100; Conservative 46; Mismatches 98; Indels 80; Gaps 12;
 QY 96 GCASQIGKKKENED-----RDFALDTDEVLYFAYVDHGHPAARD 136
 DB 130 GFTSICGRPEMEDAVSTIPFLQSSGMLDGRFDPQSAH---FFGYDGHGGSQVAN 186
 QY 137 FCHTHMEKIMDLLPKEKLN-----ETLLTFLAPLEIDKAFSSHARLSADATLLT 185
 DB 187 YCERHHLALAEIAEIAKEKPMCDGTWLEKWKALFNSFLVDSEIESVAP-----ET 239
 QY 186 SGTATVALLRGIEILVAVSGDSRAILCRKGKPKMLTDHTPERKDEKERIKCGG-FV 244
 DB 240 VGSTSVAVVFPES-HIFVANCSDRAVLRCRGKTALPLSDVHKPDREDEAARIEAAGKVI 298
 QY 245 ANNSLQPHVNGELANTRISGLDLTKTSGVIAEPE---TKRIKLHHADSEFLVLTLDGIN 301
 DB 299 QMNG-----ARVFGVLAWSRISGRYLKPS-IIPDPEVTAVRKV-----EDDCILASDGW 350
 QY 302 FMVNSQIECDFVNG-----CHDFN-----EAAHVATEQAIQVG 334
 DB 351 DVMTDEEACEMARKILLHKKNAVAGDASLLADERRKSGKDPAAAMSAEYLSKLAIQRG 410
 QY 335 TEDNSTAVVVPFGAWGKYKNSIN 358
 DB 411 SKDNISVVVDLKPRLKSKPLN 434

RESULT 3

P2C1_YEAST
 ID P2C1_YEAST STANDARD; PRT; 281 AA.
 AC P35182;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Protein phosphatase 2C homolog 1 (EC 3.1.3.16) (PP2C-1).
 GN PTC1 OR TPD1 OR YDL06W OR D2925.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetaceae; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=93360976; PubMed=8395005;
 RA Maeda T., Teai A.Y.M., Saito H.;
 RT "Mutations in a protein tyrosine phosphatase gene (PTP2) and a
 RT protein serine/threonine phosphatase gene (PTC1) cause a synthetic
 RT growth defect in Saccharomyces cerevisiae.";
 RL Mol. Cell. Biol. 13:5408-5417(1993).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=94254822; PubMed=8196609;
 RA Robinson M.K., van Zyl W.H., Phizicky E.M., Broach J.R.;
 RT "TPD1 of Saccharomyces cerevisiae encodes a protein phosphatase
 RT 2C-like activity implicated in tRNA splicing and cell separation.";
 RL Mol. Cell. Biol. 14:3634-3645(1994).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=S288C;
 RA Andre B., Vissers S., Urrestazu L.;
 RT Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE OF 167-281 FROM N.A.
 RP STRAIN=S288C / AB972;
 RA Murphy L., Richards C., Gentles S., Harris D., Barrall B.G.,
 RA Rajadream M.A.;
 RT Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: It has a serine and a weak tyrosine phosphatase activity
 CC with ratios of serine to tyrosine phosphatase activity as high as
 CC 200:1. It is essential for growth or germination at 37 degrees
 CC Celsius. May have a role in the heat shock response. Involved in
 CC tRNA splicing and cell separation.
 CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -!- COFACTOR: Binds 2 magnesium or manganese ions. Manganese is
 CC about 20 times more efficient than magnesium.
 CC -!- SIMILARITY: Belongs to the PP2C family.
 CC
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 DR EMBL; L14593; AAA34920.1; -;
 DR EMBL; Z48432; CAA8353.1; -;
 DR EMBL; Z74054; CAA98562.1; -;
 DR EMBL; Z48008; CAA88055.1; -;
 DR PIR; S41854; S41854.
 DR HSSP; P35813; IAGQ.
 DR GerMOnline; 140248; -;
 DR SGD; S0002164; PTC1.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0015071; F:protein phosphatase type 2C activity; IDA.
 DR GO; GO:0000001; P:mitochondrion inheritance; IMP.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IDA.
 DR GO; GO:0006970; P:response to osmotic stress; IGI.
 DR GO; GO:0006388; P:tRNA splicing; IMP.
 DR InterPro; IPR001932; PP2C-like.

Db 228 VQN-----RINGVLAVTRALGDTYKEL-VSAHPTTETRIWNGHDEFFIACDGLWDVV 281

QY 305 NQGEICDFNQCHDFNEAAHAYTEQAIQYGTEDNSTAVVV 344

Db 282 SQQEAADFVRFNFVSPPREAAVRLVEFALKRLSDTNITCIVV 321

RESULT 5

P2CB_RAT

ID P2CB_RAT STANDARD; PRT; 390 AA.

AC P35815; Q64046;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Protein phosphatase 2C beta isoform (EC 3.1.3.16) (PP2C-beta) (1A)

DE (Protein phosphatase 1B)

GN PPM1B OR PPM1B OR PP2C2.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Liver;

RX MEDLINE=92201367; PubMed=1312947;

RA Wenk J., Trompeter H.-I., Pettrich K.-G., Cohen P.T.W., Campbell D.G.,

RA Mieskes G.;

RT "Molecular cloning and primary structure of a protein phosphatase 2C

RT isoform";

RL PDBS Lett. 297:135-138 (1992).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Brain;

RX MEDLINE=95169115; PubMed=7532404;

RA Schafer K., Braun T.;

RT "Monoclonal anti-FLAG antibodies react with a new isoform of rat Mg2+

RT dependent protein phosphatase beta";

RL Biochem. Biophys. Res. Commun. 207:708-714 (1995).

CC -!- FUNCTION: Enzyme with a broad specificity.

CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +

CC phosphate.

CC -!- COFACTOR: Bonds 2 magnesium or manganese ions (By similarity).

CC -!- SUBUNIT: Monomer (By similarity).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Comment=Additional isoforms seem to exist. Isoforms appear to

CC differ in their C-terminus;

CC Name=1; Synonyms=Beta-1;

CC IsoId=P35815-1; Sequence=displayed;

CC Name=2; Synonyms=Beta-M2P;

CC IsoId=P35815-2; Sequence=VSP_005093;

CC -!- SIMILARITY: Belongs to the PP2C family.

CC

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CC

CC EMBL; S90449; AAB21898.1; -

CC EMBL; S74572; AAB33430.1; -

CC PIR; JC2524; JC2524.

CC PIR; S20392; S20392.

CC HSSP; P35813; 1A6Q.

CC InterPro; IPR001932; PP2C-like.

CC InterPro; IPR000222; PP2C.

CC Pfam; PF00481; PP2C; 1.

CC SMART; SM00331; PP2C SIG; 1.

CC SMART; SM00332; PP2CC; 1.

CC PROSITE; PS01032; PP2C; 1.

CC Hydrolase; Magnesium; Manganese; Multigene family;

KW

KW Alternative splicing.

FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).

FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).

FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).

FT METAL 243 243 MANGANESE 2 (BY SIMILARITY).

FT METAL 286 286 MANGANESE 2 (BY SIMILARITY).

FT VARSPLIC 379 390 GAGLEDSLVAL -> FYQSTPYSDNVSYEWQT (in isoform 2).

FT /FTId=VSP_005093.

SQ SEQUENCE 390 AA; 42889 MW; DL47615EC2FAL140B CRC64;

Query Match 16.4%; Score 319.5; DB 1; Length 390;

Best Local Similarity 31.6%; Pred. No. 2.9e-19;

Matches 94; Conservative 48; Mismatches 108; Indels 47; Gaps 10;

QY 88 PKISLENV-----GCASQISQIKRKENEDR-----PDFAQLTDEVLYEAVYDGHGQPA 134

Db 8 PKTEKNAHGAGNGRLRYGLSSMQWRVEMEDAHAVVGIPIHGLEDSWFFAVYDGHAGSRV 67

QY 135 ADFCHTHM-----EKIMDLPKKXMLETLTFLAFLEIDKAFSSHARLSADA 181

Db 68 ANYCSTHLEHITTNEEDFRAADKSGFALEPSENVKGTGRTGFKLIDVYMRNFDLRNG- 126

QY 182 TLLTSGTATVALLRDGIELVVASGDSRAILCRKGPXMKLTIDHTPERKDEKERIKKC 241

Db 127 -MDRSGSTA-VGVMISPTHYFINGDSRAVLRCRNGQVCFSTQHKPCNMEKERIQNAG 184

QY 242 GFVAWNSIQGHVNGRLAMTRISIGDLK-----TSGVIA-EPETKRIKLHHAADSFL 293

Db 185 G-----SVMIQRYNGSLAVSRALGDYDKVCDGKGPTEQLVSPPEYVEI-LRAEEDFV 238

QY 294 VLTDTGINFMVNSQICDFVQ-----CHDPNEAAHAYTEQAIQYGTEDNSTAVVVVF 346

Db 239 VLACDGIWDVMSNEELCEFYNSRLVSDLENVGVNVDVDTCLHKGSRDMSIVLCVF 295

RESULT 6

P2C4_SCHPO

ID P2C4_SCHPO STANDARD; PRT; 383 AA.

AC O14156; Q5902;

DT 15-JUL-1998 (Rel. 36, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Protein phosphatase 2C homolog 4 (EC 3.1.3.16) (PP2C-4).

GN P1C4 OR SPAC48.03C.

OS Schizosaccharomyces pombe (Fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OX NCBI_TaxID=4896;

RN [1]

RP SEQUENCE FROM N.A., SUBUNIT, SUBCELLULAR LOCATION, AND FUNCTION.

RC STRAIN=972;

RX MEDLINE=99365157; PubMed=10436019;

RA Gaits P., Russell P.;

RT "Vacuole fusion regulated by protein phosphatase 2C in fission

RT yeast";

RL Mol. Biol. Cell 10:2647-2654 (1999).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=972;

RX MEDLINE=21848401; PubMed=11859360;

RA Wood V., William R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Sgouras J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Moorey P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Skelton J., Simmonds M., Squares R., Stevens S.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Mambutt R., Purnelle B.,
 RA Gouffau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).
 CC -!- FUNCTION: Has a role in the regulation of vacuole fusion.
 CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. VACUOLAR.
 CC -!- SIMILARITY: Belongs to the PP2C family.
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 CC EMBL; AF140285; AAD27651.1; -.
 CC EMBL; Z98762; CAB58554.1; -.
 CC FIC; T38772; T38772.
 CC GeneDB Spombe; SPAC4A8.03c; -.
 CC InterPro; IPR001932; PP2C-like.
 CC InterPro; IPR000222; PP2C.
 CC Pfam; PF00481; PP2C; 1.
 CC SMART; SM00331; PP2C_SIG; 1.
 CC SMART; SM00332; PP2C; 1.
 CC PROSITE; PS01032; PP2C; 1.
 CC Hydrolase; Magnesium; Manganese; Membrane; Multigene family.
 KW METAL 92 92 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL 308 308 MANGANESE 2 (BY SIMILARITY).
 FT METAL 347 347 MANGANESE 2 (BY SIMILARITY).
 FT METAL 363 363 MANGANESE 2 (BY SIMILARITY).
 SEQUENCE 363 AA; 43569 MW; 85E00C2BDAE4B9BF CRC64;
 Query Match 15.9%; Score 310.5; DB 1; Length 383;
 Best Local Similarity 28.5%; Pred. No. 1.6e-18;
 Matches 93; Conservative 52; Mismatches 118; Indels 63; Gaps 10;
 QY 86 PIPKSL---ENVGASQIGKREKEDRDFPAQLT-----DEVLYFAVYDGGGPA 133
 Db 39 PYLKISMKAPQSGLCTARGDSFTNQDRMAYGYLANLKDTTDRSDSPFFGLFDGGTGE 98
 QY 134 AADFCHTHMEKCI--MDLLPKKKNLETL----- 159
 Db 99 CSEFLSTNLGIIINQDINDTEKILKEVSHVSGYMGAKPKPPFLRTVLQSRDEDLWRAR 158
 QY 160 LTLAFLETDKAF--SSHARLSADATLLTSGTTATVALL-----RDGIELVVASVGD 208
 Db 159 LYYSFLQADMVLYNARSPDSAV--PGAVGTVAITTSKNLSYVESDSYIIHLAVGD 216
 QY 209 SRAILC--RKQPKMLTIDHTPERKDEKRIKCGGFVAMNSLGQPHVNGKLAWTSIGD 266
 Db 217 TRALLCDSTRGHRHLTFQHPADVEARLRRLRYNMGFSRDSFGQKRF--AWVANTSFGD 275
 QY 267 -LDLKTSGVIAPEPTKILHHADDSEVLVTTTGTFNFMNSQELICDPVNOCHPNEAHA 325
 Db 276 GYLUKUGVNAEPOLTSIHSURDWSFLTLLSDGITDVSDDVDVLIKLSESPPQAAAN 335
 QY 326 VTEQAIQYGTEDNSTAVVVPFGAWGK 351

Db 336 IIRYAQNVGAVDITCLVVRPLFGMKK 361
 RESULT 7
 P2CA_BOVIN STANDARD; PRT; 382 AA.
 ID P2CA_BOVIN
 AC O62829;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha).
 GN PPM1A.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=98146173; PubMed=9486768;
 RA Klump S., Selke D., Fischer D., Baumann A., Mueller F., Thanos S.;
 RT "Protein phosphatase type-2C isozymes present in vertebrate retinae:
 RT purification, characterization, and localization in photoreceptors.";
 RL J. Neurosci. Res. 51:328-338(1998).
 CC -!- FUNCTION: Enzyme with a broad specificity.
 CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -!- COFACTOR: Binds 2 magnesium or manganese ions.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SIMILARITY: Belongs to the PP2C family.
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 CC
 CC EMBL; A005457; CAA06554.1; -.
 CC HSP; P35813; IAGQ.
 CC InterPro; IPR001932; PP2C-like.
 CC InterPro; IPR000222; PP2C.
 CC Pfam; PF00481; PP2C; 1.
 CC SMART; SM00331; PP2C_SIG; 1.
 CC SMART; SM00332; PP2C; 1.
 CC PROSITE; PS01032; PP2C; 1.
 CC Hydrolase; Magnesium; Manganese; Multigene family.
 KW METAL 37 37 MANGANESE 1 (BY SIMILARITY).
 FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
 FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL 239 239 MANGANESE 2 (BY SIMILARITY).
 FT METAL 282 282 MANGANESE 2 (BY SIMILARITY).
 SEQUENCE 382 AA; 42529 MW; A716B3FA0E7E21C2 CRC64;
 Query Match 15.8%; Score 307.5; DB 1; Length 382;
 Best Local Similarity 31.0%; Pred. No. 2.8e-18;
 Matches 91; Conservative 43; Mismatches 115; Indels 45; Gaps 10;
 QY 88 PKISLNV-----CCASQIGKREKEDR-----PDFAQLTDEVLYFAVYDGGGPA 134
 Db 8 PWEKXNAQGGNGLRYGLSSNQGRVNEADHATVIGLPSGLTWSFFAVYDGHASQV 67
 QY 135 ADFCHTHMEKIMDL-----LPKERNLETLTLTFLAFLEIDK--AFSSHARLSADATLL 184
 Db 68 AKYCCHELLDHTNNQDFKGSAGAPSVENVKNGIRTGTGLEIDHMRVMSKKHAD--- 123
 QY 185 TSGTATTALLRDGIELVVASVGSRAILCRKGFPMKLTIDHTPERKDEKRIKCGGFV 244
 Db 124 RSGSTA--VGVLISPOHTVYFNGDSRGLLCRNRYVFTQDHKPSNPLEKRIQAGG-- 180
 QY 245 AWNSLGQPHVNGRLNATRSIGDLDLK-----TSGVIA--EPETKRIKLHADDSEVLVLT 296

```

Db 181 ---SVMQIRVNGSLAVSALGDFDYKCVHGKPTQLVSPPEVHDIERSEDDQFIILA 237
QY 297 TDGINFMVNSQICDFVQVQ-----CHDPNEAAHAYTEQAIQYGTEDNSTAVVVPF 346
Db 238 CDGIWDMVNGNEELCDFVRSLEVRLEVTDDLEKVCNEVVDTCLYKGRDNMSVILICF 291

RESULT 8
P2CA HUMAN
ID P2CA HUMAN STANDARD; PRT; 382 AA.
AC P35813; 075551;
DT 01-JUN-1994 (Rel. 29, Created)
DT 10-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (P2C-alpha) (TA)
DE (protein phosphatase 1A).
GN PPM1A OR PPM1A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA-1).
RX MEDLINE=92182001; PubMed=1311954;
RA Mann D.J., Campbell D.G., McGowan C.H., Cohen P.T.W.;
RT "Mammalian protein serine/threonine phosphatase 2C: cDNA cloning and
RT comparative analysis of amino acid sequences.";
RL Biochim. Biophys. Acta 1130:100-104(1992).
[2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA-2).
RX MEDLINE=98372738; PubMed=9707433;
RA Takakawa M., Maeda T., Saito H.;
RT "Protein phosphatase 2Calpha inhibits the human stress-responsive p38
RT and JNK MAPK pathways.";
RL EMBO J. 17:4744-4752(1998).
[3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA-1).
RC TISSUE=Colon; PubMed=12477932;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:15899-15903(2002).
[4]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE=97157470; PubMed=9003755;
RA Das A.K., Helps N.R., Cohen P.T.W., Barford D.;
RT "Crystal structure of the protein serine/threonine phosphatase 2C at
RT 2.0-A resolution.";
RL EMBO J. 15:6798-6809(1996).
CC -!- FUNCTION: Enzyme with a broad specificity.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- COFACTOR: Binds 2 magnesium or manganese ions.
CC -!- SUBUNIT: Monomer.
CC -!- ALTERNATIVE PRODUCTS:

```

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CC CC Event=Alternative splicing; Named isoforms=2;
CC CC Name=Alpha-1;
CC CC IsoId=P35813-1; Sequence=Displayed;
CC CC Name=Alpha-2;
CC CC IsoId=P35813-2; Sequence=VSP_005085, VSP_005086;
CC CC -!- SIMILARITY: Belongs to the P2C family.
CC CC
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CC CC or send an email to license@isb-sib.ch).
CC CC
CC CC EMBL; S8759; AAC21784.1; -
CC CC EMBL; AF070670; AAC28354.1; -
CC CC EMBL; BC026691; AAC26691.1; -
CC CC PIR; S22423; S22423.
CC CC Genew; HGNC:9275; PPM1A.
CC CC MIN; 606108; -
CC CC PDS; 1A6Q; 27-MAY-98.
CC CC GO; GO:0015071; F:protein phosphatase type 2C activity; TAS.
CC CC InterPro; IPR001932; P2C-like.
CC CC InterPro; IPR000222; P2C.
CC CC Pfam; PF00481; P2C; 1.
CC CC SMART; SM00331; P2C_SIG; 1.
CC CC SMART; SM00332; P2C_C; 1.
CC CC PROSITE; PS01032; P2C; 1.
CC CC HydroLase; Magnesium; Manganese; Multigene family;
CC CC Alternative splicing; 3D-structure.
CC CC METAL 37 37 MANGANESE 1.
CC CC METAL 38 38 MANGANESE 1.
CC CC METAL 60 60 MANGANESE 1 AND 2.
CC CC METAL 239 239 MANGANESE 2.
CC CC METAL 282 282 MANGANESE 2.
CC CC METAL 318 324 EIIKKQG -> GGSFNKK (in isoform Alpha-2).
CC CC VARSPLIC 325 382 Missing (in isoform Alpha-2).
CC CC VARSPLIC 325 382 /FTid=VSP_005086.
CC CC
CC CC STRAND 9 19
CC CC TURN 20 21
CC CC STRAND 22 31
CC CC TURN 32 32
CC CC STRAND 38 46
CC CC TURN 47 49
CC CC STRAND 50 62
CC CC TURN 81 81
CC CC TURN 83 86
CC CC HELIX 94 118
CC CC TURN 119 120
CC CC STRAND 126 127
CC CC STRAND 129 134
CC CC STRAND 138 144
CC CC STRAND 148 153
CC CC TURN 154 155
CC CC STRAND 156 160
CC CC TURN 166 167
CC CC TURN 169 177
CC CC TURN 178 179
CC CC STRAND 182 183
CC CC TURN 184 185
CC CC STRAND 186 187
CC CC TURN 188 190
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CC CC STRAND 216 216
CC CC STRAND 220 225

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FT TURN 228 230
 FT STRAND 231 237
 FT HELIX 239 242
 FT TURN 243 244
 FT HELIX 247 258
 FT TURN 259 260
 FT HELIX 264 277
 FT TURN 278 279
 FT STRAND 284 290
 FT TURN 292 293
 FT HELIX 299 319
 FT HELIX 330 339
 FT TURN 340 341
 FT TURN 347 349
 FT HELIX 350 354
 FT HELIX 355 365
 SQ SEQUENCE 382 AA; 42447 MW; D48EF508B4A76687 CRC64;

Query Match 15.8%; Score 307.5; DB 1; Length 382;
 Best Local Similarity 31.0%; Pred. No. 2.8e-18;
 Matches 91; Conservative 43; Mismatches 115; Indels 45; Gaps 10;

QY 88 PKISLENV-----GCAQIGKREKEDR----PDFALTDVLYFAVYDCHGGPAA 134
 DB 8 PMEKHNAQGGNGRLYGLSSNQGRVEMEDAHTAVIGLPSGLSWFFFAVYDGHAGSQV 67
 QY 135 ADFCHTHMEKIMDL-----LPKKNLETLTLTFLAFLDK--AFSSHARLSADATLL 184
 DB 68 AKYCCHELLDHTNNQDFKGSAGAPSVENVKNGIRGTGFLDEHWRVNSEKHCAD---- 123
 QY 195 TSGTATVALRDGIELVAVGDSRAILCRKGPMLTIDHTPERKDEKERIKKCGGFV 244
 DB 124 RSGSTA-VGVLSIPQHTYFNCGRSGLLRKRVHFEFTQDKFSPNLEKRIQAGG-- 180
 QY 245 AwnSLGQPHVNGRLAMTRISIGDLK-----TSGVIA-EPETKRIKLHADDSDFLVLT 296
 DB 181 ---SVMIQRVNSGLAVSRALGDFDYKCVHGKGPTEQLVSPPEVHDIERSEEDDQFIILA 237
 QY 297 TDGTFNFMVNSOICDFVNVQ-----CHDNEAAHAYTEQAIQVGTEDNSTAVVWPF 346
 DB 238 CDGIWDVNGNEELCDFVRSLREVTDDLEKVCNEVVDTCLYKGRDNMSVLICF 291

RESULT 9

P2CB_MOUSE STANDARD; PRT; 390 AA.

AC P2CB_MOUSE
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Protein phosphatase 2C beta isoform (EC 3.1.3.16) (P2C-beta) (IA)
 DE (Protein phosphatase 18).
 GN PPMIB OR PPMIB OR PPMIB OR PPMIB
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94099616; PubMed=8274020;
 RA Terasawa T., Kobayashi T., Murakami T., Ohnishi M., Kato S.,
 RA Kato S., Terasawa T., Kobayashi T., Takeuchi T., Tamura S.,
 RA Tanaka O., Kondo H., Yamamoto H., Yamamoto H., Hiraga A., Matsui Y.,
 RT "Molecular cloning of a novel isotype of Mg(2+)-dependent protein
 RT phosphatase beta (type 2C beta) enriched in brain and heart.";
 RL Arch. Biochem. Biophys. 307:342-349(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (BETA-3, BETA-4 AND BETA-5).
 RC TISSUE=Testis;
 RX MEDLINE=95251388; PubMed=7733667;
 RA Kato S., Terasawa T., Kobayashi T., Ohnishi M., Sasahara Y.,
 RA Kusuda K., Yanagawa Y., Hiraga A., Matsui Y., Tamura S.,
 RT "Molecular cloning and expression of mouse Mg(2+)-dependent protein
 RT phosphatase beta-4 (type 2C beta-4).";

RL Arch. Biochem. Biophys. 318:387-393(1995).
 RN [3]
 RP SEQUENCE FROM N.A. (BETA-3 AND BETA-4).
 RC TISSUE=Testis;
 RX MEDLINE=94313028; PubMed=8038726;
 RA Hou E.W., Kawai Y., Miyasaka H., Li S.S.;
 RT "Molecular cloning and expression of cDNAs encoding two isoforms of
 RT protein phosphatase 2C beta from mouse testis.";
 RL Biochem. Mol. Biol. Int. 32:773-780(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=99398339; PubMed=10469137;
 RA Ohnishi M., Chida N., Kobayashi T., Wang H., Ikeda S., Hanada M.,
 RA Yanagawa Y., Katsura K., Hiraga A., Tamura S.;
 RT "Alternative promoters direct tissue-specific expression of the mouse
 RT protein phosphatase 2C beta gene.";
 RL Eur. J. Biochem. 263:736-745(1999).
 CC -!- FUNCTION: Enzyme with a broad specificity.
 CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=5;
 CC Comment=Isoforms only differ in their C-terminus;
 CC Name=Beta-1;
 CC IsoId=P36993-1; Sequence=Displayed;
 CC Name=Beta-2;
 CC IsoId=P36993-2; Sequence=VSP_005089;
 CC Name=Beta-3;
 CC IsoId=P36993-3; Sequence=VSP_005090;
 CC Name=Beta-4;
 CC IsoId=P36993-4; Sequence=VSP_005091;
 CC Name=Beta-5;
 CC IsoId=P36993-5; Sequence=VSP_005092;
 CC -!- TISSUE SPECIFICITY: Beta-1 is expressed ubiquitously; beta-2 is
 CC expressed exclusively in brain and heart; beta-4 is expressed
 CC exclusively in brain and intestine; beta-3 and beta-5 are
 CC expressed exclusively in testis and intestine.
 CC -!- SIMILARITY: Belongs to the P2C family.
 CC
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 CC EMBL; D17411; BAA04233.1; -
 CC EMBL; D17412; BAA04234.1; -
 CC EMBL; D45859; BAA08293.1; -
 CC EMBL; D45860; BAA08294.1; -
 CC EMBL; D45861; BAA08295.1; -
 CC EMBL; U09218; AAB60442.1; -
 CC EMBL; AB007798; BAA84471.1; -
 CC EMBL; AB007794; BAA84471.1; JOINED.
 CC EMBL; AB007795; BAA84471.1; JOINED.
 CC EMBL; AB007796; BAA84471.1; JOINED.
 CC EMBL; AB007797; BAA84471.1; JOINED.
 CC PIR; I49016; I49016.
 CC PIR; S65672; S65672.
 CC HSP; P35813; IACQ.
 CC XGD; MG1:101841; Ppmib.
 CC InterPro; IPR001932; P2C-like.
 CC InterPro; IPR000222; P2C.
 CC Pfam; PF00481; P2C; 1.
 CC SMART; SM00331; P2C SIG; 1.
 CC SMART; SM00332; P2CC; 1.
 CC PROSITE; PS01032; P2C; 1.
 CC Hydrolase; Magnesium; Manganese; Multigene family;
 CC Alternative splicing.
 KW

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FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL 243 243 MANGANESE 2 (BY SIMILARITY).
FT METAL 286 286 MANGANESE 2 (BY SIMILARITY).
FT VARSPLIC 379 390 GAGDLEDSLVLA -> VSLHLPKYLK (in isoform Beta-2).
FT VARSPLIC 379 390 /FTID=VSP 005089.
FT VARSPLIC 379 390 GAGDLEDSLVLA -> FYQPSIAYSDNNVFL (in isoform Beta-3).
FT VARSPLIC 379 390 /FTID=VSP 005090.
FT VARSPLIC 379 390 GAGDLEDSLVLA -> MADLSTICKPS (in isoform Beta-4).
FT VARSPLIC 379 390 /FTID=VSP 005091.
FT VARSPLIC 379 390 VAL -> FYQPSIAYSDNNVFL (in isoform Beta-5).
FT VARSPLIC 379 390 /FTID=VSP 005092.
FT SEQUENCE 390 AA; 42795 MW; 255C97B4276189FD CRC64;
Query Match 15.7%; Score 307.5; DB 1; Length 390;
Best Local Similarity 31.0%; Pred. No. 2.9e-18;
Matches 92; Conservative 48; Mismatches 110; Indels 47; Gaps 10;
QY 88 PKISLENV-----GCASQIGKRENERD-----FDPALQTDVLYFAYVDGSGPAA 134
DB 8 PATEKHNAHAGNGLRYGLSSMQGWRVEMDAHTAVGIPHLDNWSFFAYVDGHAGSRV 67
QY 135 ADFCHTHM-----SKCMIDLPEKKNLETLTLAFLEIDKAFSHARLSADA 181
DB 68 ANVCSTHLEHTITNEDFRAADKSGSALEPSVESVKTGRTGLKIDEMRNFSLRNG- 126
QY 182 TLLTSGTTATVALLRDGIELVVASGDSRAILCRKQPKMLTIDHTPERKDEKRIKCG 241
DB 127 -MDRSGSTA-VGMVSPHTNYFINCDSRAVLCRNGQVCFTQDKHPCNPVEKERIQNAG 184
QY 242 GFVAMNSLGQPHVNGSLAMTRISGDLDLK-----TSGVIA-EPETKRIKLHADDNFL 293
DB 185 G-----SVMIQVNGSLAVSRALGDYDKVCGKGTQELVSPPEVVEI-VRABEDSFV 238
QY 294 VLTTDGINFMVNSQELCDFVQ-----CHDPNEAAHVAITEQATQYCTEDNSTAVVVF 346
DB 239 VLACDGIWDMNSBELCEFKRLEVSDDLENNVGNVVDTCCLKHGRDNNNSVLLVCF 295

RESULT 10
P2CA_MOUSE
ID P2CA_MOUSE STANDARD; PRT; 382 AA.
AC P4943;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha) (IA)
DE (Protein phosphatase 1A).
GN PPM1A OR PPM1A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94333828; PubMed=8056349;
RA Kato S., Kobayashi T., Terasawa T., Ohnishi M., Sasahara Y.,
RA Kanamaru R., Tamura S.;
RT "The cDNA sequence encoding mouse Mg2+ -dependent protein phosphatase
RT alpha."
RL Gene 145:311-312(1994).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
```

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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Rubin A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Enzyme with a broad specificity.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- COFACTOR: Binds 2 magnesium or manganese ions.
CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: Belongs to the PP2C family.
CC
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CC
CC -----
CC EMBL; D28117; BAA05662.1; --
CC EMBL; BC008595; AA08595.1; --
CC F01; 153823; 153823.
CC HSSP; P35813; 1A6Q.
CC MGI; 99878; Ppmla.
CC InterPro; IPR001932; PP2C-like.
CC MGD; MGI:99878; Ppmla.
CC InterPro; IPR000222; PP2C.
CC Pfam; PF00481; PP2C; 1.
CC SMART; SM00331; PP2C_SIG; 1.
CC SMART; SM00332; PP2CC; 1.
CC PROSITE; PS01032; PP2C; 1.
CC Hydrolase; Magnesium; Manganese; Multigene family.
FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL 239 239 MANGANESE 2 (BY SIMILARITY).
FT METAL 282 282 MANGANESE 2 (BY SIMILARITY).
FT SEQUENCE 382 AA; 42432 MW; DC206610B1583870 CRC64;
Query Match 15.7%; Score 306.5; DB 1; Length 382;
Best Local Similarity 31.0%; Pred. No. 3.4e-18;
Matches 91; Conservative 43; Mismatches 115; Indels 45; Gaps 10;
QY 88 PKISLENV-----GCASQIGKRENERD-----FDPALQTDVLYFAYVDGSGPAA 134
DB 8 PATEKHNAHAGNGLRYGLSSMQGWRVEMDAHTAVGIPHLDNWSFFAYVDGHAGSRV 67
QY 135 ADFCHTHMCKIMDL-----LPKKNLETLTLAFLEIDK--AFSSHARLSADATLL 184
DB 68 AKYCCHELLDHTNNQDFRSGAGAPSVENVNGIRTGFEIDEMRVMSKKHGAD---- 123
QY 185 TSGTTATVALLRDGIELVVASGDSRAILCRKQPKMLTIDHTPERKDEKRIKCGFV 244
DB 124 RSGSTA-VGVLTSPQHTYFINGDSRGLLCNRKVHFFTDQHKPSNPLEKERIQNAG-- 180
QY 245 AMNSLGQPHVNGSLAMTRISGDLDLK-----TSGVIA-EPETKRIKLHADDNFLVLT 296
DB 181 ----SVMIQVNGSLAVSRALGDYDKVCGKGTQELVSPPEVVEIERSBEDDQFIILA 237
QY 297 TDGINFMVNSQELCDFVQ-----CHDPNEAAHVAITEQATQYCTEDNSTAVVVF 346
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Db 68 AKYCEHLDHITNQDFKSGAGAPSVENKNGTGTGLEIDEHVMVSEKKGAD-----123
QY 185 TSGTTATVALLRDGIELVAVSGDSRAILCRKGPMLTIDHTPERKDEKERIKKCGFV 244
Db 124 RSGSTA-VGVLSIPQHTFYINGDSRGLLCKNRKVHFFTDQHKPSNPLEKERIQWAGG--180
QY 245 AWNSLQGVHNGRIAMTSGIDLDLK-----TSGVIA-EPETKRIKLHADDSEFLVLT 296
Db 181 ---SVNIORVNGSLAVSRALGDFYKCVHGKPTQLVSPPEVHDIERSEDDQFILA 237
QY 297 TDGINFMVNSOICDFVQ-----CHDPNEAAHVAITEQAIOYGTEDNSTAVVVF 346
Db 238 CDGIWDVNGNEBELCDFVSRLEVTDDLEKVCNEVVDTCLYKGRDNMSVILICF 291

RESULT 13
ID P2C3 SCHPO STANDARD; PRT; 414 AA.
AC Q09173;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein phosphatase 2C homolog 3 (EC 3.1.3.16) (PP2C-3).
GN PTC3 OR SPAC2G11.07C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=95163582; PubMed=7859738;
RA Shiozaki K., Russell P.;
RT "Counteractive roles of protein phosphatase 2C (PP2C) and a MAP
RL kinase kinase homolog in the osmoregulation of fission yeast.";
RL ENBO J. 14:492-502 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth I., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy S., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
RA Welter J., Vansteels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Sipakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RN Nature 415:871-880 (2002).
CC -!- FUNCTION: Has an important role in osmotic stability and cell
CC shape control. It may negatively regulate the osmosensing signal
CC transmitted through wsl1 map kinase.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.

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CC -!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: Belongs to the PP2C family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L34882; AAA67321.1; --
CC EMBL; Z54354; CAA91172.1; --
CC PIR; T38573; S62462.
CC HSP; P35813; IA60.
CC GeneDB SPombe; SPAC2G11.07c; --
CC InterPro; IPR001932; PP2C-like.
CC InterPro; IPR000222; PP2C.
CC Pfam; PF00481; PP2C; 1.
CC SMART; SM00331; PP2C_Sig; 1.
CC SMART; SM00332; PP2C; 1.
CC PROSITE; PS01032; PP2C; 1.
CC K0 Hydrolyase; Magnesium; Manganese; Multigene family.
CC FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
CC FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
CC FT METAL 62 62 MANGANESE 1 AND 2 (BY SIMILARITY).
CC FT METAL 230 230 MANGANESE 2 (BY SIMILARITY).
CC FT METAL 279 279 MANGANESE 2 (BY SIMILARITY).
CC FT CONFLICT 196 196 K -> T (IN REF. 1).
CC SQ SEQUENCE 414 AA; 44856 MW; EBF3A416625A2B11 CRC64;

Query Match 15.7%; Score 306.5; DB 1; Length 414;
Best Local Similarity 33.1%; Pred. No. 3.8e-18; Indels 55; Gaps 12;
Matches 97; Conservative

QY 96 GCASQIGKRKENED-----RFDPAQLTDELYFAVYDGHGGFAAADPCHTHMEKIMDL 149
Db 25 GLSSWQWRISMEDAHSAILSMCECAVKKDPVDFVYDGHGGKVAKWCNSLPPQIL-- 81
QY 150 LPKKNLE-----TLTLTAFLEIDKAFSHARLSADATLLTSGTTATVALLRDGIELV 202
Db 82 ---EKNPDFQKGFVNALKSFLNADRAILLDDQGFHTD---PSGCTATV-VLRVGNKLY 133
QY 203 VASVGDGRAILCRKGPMLTIDHTPERKDEKERIKKCGFVAVNSLQGFHVNGRLAMTR 262
Db 134 CANAGDSRTVLGSGIAKPLSADHKPSNEAEKARICAAAGFVDFG----RVNGNLALSR 188
QY 263 SIGDLDLTSGTVIAEPETK-----RIKLHHA--DPSFLVLTDTGTFMWNVNSOICDFVN 314
Db 189 AIGDFEPKSNL--EPEKQIVTALPVDVVVHEITDDDEFVLACDGIWDCKTSQVIEFVR 246
QY 315 Q-----CHDPNEAAHVAITEQAIOYGT-----DNSTAVVVF-----GANGK 351
Db 247 RGIVAGTSLERIAENMDNCIASDTETGLCDNMTVCIVALLQENDKSANYK 299

RESULT 14
ID P2C2 SCHPO STANDARD; PRT; 370 AA.
AC Q09172;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein phosphatase 2C homolog 2 (EC 3.1.3.16) (PP2C-2).
GN PTC2 OR SPCC1223.11.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.

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DD
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K

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 12, 2004, 05:55:18 ; Search time 36 Seconds
(without alignments)
993.979 Million cell updates/sec

Title: US-10-716-488-2
Perfect score: 1951
Sequence: 1 MSTAAALTLVRSGNQVRR.....KNSEINFSSRSFASGRWA 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	360	18.5	348	2 T50783	protein phosphatas
2	357	18.3	383	2 T48018	hypothetical prote
3	344.5	17.7	392	2 F84650	probable protein p
4	338	17.3	434	2 T04263	phosphoprotein pho
5	337.5	17.3	381	2 T03640	protein phosphatas
6	332.5	17.0	359	2 T52337	phosphoprotein pho
7	328	16.8	362	2 F84695	probable protein p
8	326	16.7	464	2 H96700	protein F12A21.5 (
9	325	16.7	281	2 S41854	phosphoprotein pho
10	322.5	16.5	239	2 T01361	probable protein p
11	322.5	16.5	816	2 T48123	hypothetical prote
12	322	16.5	511	2 F96752	protein phosphatas
13	321.5	16.5	347	2 A56058	phosphoprotein pho
14	320	16.4	355	2 H84643	probable protein p
15	319.5	16.4	389	2 T05095	hypothetical prote
16	319.5	16.4	290	2 S20392	phosphoprotein pho
17	319.5	16.4	397	2 JC3524	phosphoprotein pho
18	318.5	16.3	423	2 T48121	hypothetical prote
19	318	16.3	238	2 D96811	hypothetical prote
20	311.5	16.0	361	2 T45778	protein phosphatas
21	310.5	15.9	383	2 T38772	protein phosphatas
22	307.5	15.8	382	2 S22423	phosphoprotein pho
23	307.5	15.8	390	2 S65672	phosphoprotein pho
24	307.5	15.8	393	2 T49016	phosphoprotein pho
25	307.5	15.8	396	2 T02483	probable protein p
26	306.5	15.7	382	2 I53823	magnesium dependen
27	306.5	15.7	382	2 S22422	phosphoprotein pho
28	306.5	15.7	382	2 A32399	phosphoprotein pho
29	306.5	15.7	414	2 S62462	protein phosphatas

30	305	15.6	370	2 S54297	protein phosphatas
31	304	15.6	404	2 T00750	probable protein p
32	304	15.6	442	2 B86209	protein F22G5.22 (
33	301	15.4	357	2 T06308	protein phosphatas
34	301	15.4	1428	2 T13926	probable protein p
35	300.5	15.4	300	2 A55804	phosphoprotein pho
36	288.5	14.8	268	2 T04610	protein phosphatas
37	288	14.8	281	2 F86355	T16S15.10 protein
38	287.5	14.7	242	2 T18588	probable protein p
39	285.5	14.6	290	2 E84591	probable protein p
40	285.5	14.6	380	2 E84748	phosphoprotein pho
41	281	14.4	399	2 S55457	phosphoprotein pho
42	279	14.3	406	2 A47492	phosphoprotein pho
43	278.5	14.3	405	2 F86206	hypothetical prote
44	278.5	14.3	514	2 D84584	probable protein p
45	278	14.2	348	2 E88434	protein T23F11.1 (

ALIGNMENTS

RESULT 1

T50783
protein phosphatase 2C-like protein - Arabidopsis thaliana
N;Alternate names: protein T30N20_10
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 15-Jun-2001
C;Accession: T50783
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirksen, W.; Stiekema, W.; Bancroft, I.; Mew

A;Reference number: Z25240
A;Accession: T50783
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-348 <BEV>
A;Cross-references: EMBL:AL365234
A;Experimental source: cultivar Columbia; BAC clone T30N20
C;Genetics:
A;Map position: 5
A;Introns: 27/2; 70/1; 103/1; 156/1; 185/1; 209/3; 234/3
A;Note: T30N20_10
C;Superfamily: human phosphoprotein phosphatase 1A

Query Match 18.5%; Score 360; DB 2; Length 348;
Best Local Similarity 35.4%; Pred. No. 1e-22;
Matches 99; Conservative 56; Mismatches 89; Indels 36; Gaps 11;

QY	96	GCASQIGKRNEDRD--FAQLTDEVL-YFAYVDGGGPAADFCHTHMEKIMDLPK	152
DB	35	GYASSAGKRSMDFFETRIDGGEIVGLFVDFGHHGARAAYVVRHL---	FSNLITH 91
QY	153	EK---NLETLITLAFLEID---KAFSSHARLSADATLLTSGTTATVALLRDGIELVVAS	205
DB	92	PKFISDTKSAITDAYNHTDSELLKSENSNR-----DAGSTASTAIL-VGDRLVVAN	142
QY	206	VGDSRAILCRGKPKMLTIDHTPERKDEKRIKCGGFVAVNSLGQFVNGRLAMTSSIG	265
DB	143	VGDSRAVISGGKAIVSRDHKPDQSDERERIENAGGFVNW-----AGVLAVSRAFG	194
QY	266	DLDLTKGVAEPETKIKLHADDSS--FLVLITDGINFVNSQEI CDFVNCQCHDPNEAA	323
DB	195	DRLLK-QYVVADPIQEKI---DDTLFLILASDLGWDVFSNEAAVAMVKEVEDPDSA	250
QY	324	HAVTEQAIQYGTENSTAVVPPFGAWGKYKNSEINFESR	363
DB	251	KKLVGGAIKRGSADNITCVVVRVFLKKSSASSHSSSSK	290

RESULT 2

T48018
hypothetical protein T17J13.220 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

[illegible]

QY 335 TEDNSTAVVPFGANGKYKSEIN 358
Db 411 SKDNISVVVVDLKPRLKSKPLN 434

RESULT 5
T09640
protein phosphatase 2C - alfalfa
C:Species: Medicago sativa (alfalfa)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T09640
R:Meskine, I.; Boegre, L.; Glaeser, W.; Brandstoetter, M.; Zwerger, K.; Ammerer, G.; Hir
Proc. Natl. Acad. Sci. U.S.A. 95, 1938-1943, 1998
A:Title: MP2C, a plant protein phosphatase 2C, functions as a negative regulator of mito
A:Reference number: Z16791; MUID:98132696; PMID:9465121
A:Accession: T09640
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-381 <MES>
A:Cross-references: EMBL:Y11607; NID:G2582799; PIDN:CAA72341.1; PID:G2582800
C:Genetics:
A:Gene: MP2C

Query Match 17.3%; Score 337.5; DB 2; Length 381;
Best Local Similarity 33.3%; Pred. No. 9.6e-21;
Matches 87; Conservative 51; Mismatches 90; Indels 33; Gaps 11;

QY 102 GKRKENEDRFDA---QLTDEVLYFAVVDGCGPAAADFCHTHMEKCMD--LLPKKKNL 156
Db 134 GAREYMERDRTAGVNLRENNLAFGVDFGCGAKAFARNLEKNILDEVITDEDDV 193

QY 157 ETLTFLAFLEIDKAFSHARLSADATLITSGTTATVALLRDLGIELVWASVGDSEILCRK 216
Db 194 EBAVRKGYLNTDSEF---MKKD---LHGGSCCVTAFIRNG-NLVWSNAGDCRAVISRG 244

QY 217 GKPKMLTIDHTPERDEXERIKKCGGFV-----ANSLGQPHVNGRLAMTSGIDLDLKT 271
Db 245 GVAELTSDHRSRDEKDRITLGGYDLRCGVW-----RIQGLAVSRGIGDRHLK- 297

QY 272 SGVIAEPETRIKLHADDSPFLVLTDTGGINFMVNSQIEICDFVQ-C-----HDPNEAAHA 325
Db 298 QWVTAEPETKIRIPEHD-LLILASDGLWQVNSQIEAVDIARQFCVGNQNNQPLMACKK 356

QY 326 VTEQAIQVGTENDNSTAVVVPF 346
Db 357 LAQLSVSRGSLDTSVMIKF 377

RESULT 6
T22337
phosphoprotein phosphatase (EC 3.1.3.16) 2C [imported] - common ice plant
C:Species: Mesembryanthemum crystallinum (common ice plant)
C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 01-Mar-2002
C:Accession: T52337
R:Miyazaki, S.; Koga, R.; Bohnert, H.J.; Fukuhara, T.
Mol. Gen. Genet. 261, 307-316, 1999
A:Title: Tissue- and environmental response-specific expression of 10 PP2C transcripts
A:Reference number: Z26045; MUID:199200489; PMID:10102366
A:Accession: T52337
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-359 <MIY>
A:Cross-references: EMBL:AF075580; PIDN:AAC36698.1
C:Genetics:
A:Gene: PP2C
C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.220
C:Keywords: phosphoric monoester hydrolase

Query Match 17.0%; Score 332.5; DB 2; Length 359;
Best Local Similarity 29.8%; Pred. No. 2.3e-20;
Matches 100; Conservative 60; Mismatches 107; Indels 69; Gaps 14;

QY 47 GSRFD---PDGSGSPATWDFGWDNRIDEPIL-LPPSIKYKPIPKISLENVGCASQIG 102

Db 22 CSOLDIMTPD-----AVSDNLSASTMLQFVNIRSGS-----FADIG 58
QY 103 KRKENED---RFD-----FAQLTDEVLYFAVVDGCGPAAADFCHTHMEKCMD--L 149
Db 59 PRKYMEDEHRIIDLSVQLGSLFRCPKSAFYGVDFGCGSEAAAYRVENVRFFEDVS 118
QY 150 LPKKNL-----ETLLTFLAFLEIDKAFSHARLSADATLITSGTTATVALLRDLGIEL 201
Db 119 FPASELDIFLEGVENCRRRAFFLADLADDCSIST-----SSGTTALTALVL-GRLL 172
QY 202 VVASVGDSEILCRKPKMLTIDHTPERKDKERIKKCGGFVWVNSLQPHVNGRLAMT 261
Db 173 LVNAGDCRAVLCKRGEADMSQDHRTPTYPEKRRVEELGGVY-----DDGLNGVLVS 227
QY 262 RSIGDLDLK-----TSGVIAEPETRIKLHADDSPFLVLTDTGGINFMVNSQIEICDFV 313
Db 228 RALGDWDMKLPKGSASPLISEPELROIITE-DDEFLIIGCDGIWDVVISQQAVSIVRWG 286
QY 314 -NOCHDPNEAAHVAVTEQAIQVGTENDNSTAVVVPFGA 348
Db 287 LKRHDDPEQSAKDLVNEALRRHTIDNLTVIIVCFSS 322

RESULT 7
F84695
probable protein phosphatase 2C [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: F84695
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Varakan, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: F84695
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-362 <STO>
A:Cross-references: GB:AE002093; NID:G3980397; PIDN:AAC95200.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g29380
A:Map position: 2
C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.220

Query Match 16.8%; Score 328; DB 2; Length 362;
Best Local Similarity 28.9%; Pred. No. 5.7e-20;
Matches 108; Conservative 59; Mismatches 119; Indels 88; Gaps 18;

QY 18 RRRVLLSSRLQLDQDRRVPTCHSTSEPRCSRFPDPSGSGSP-ATWDFGWDNRIDEPIL 76
Db 26 RRRPRFQTVMHEDWEK---NCKSKQELALAIR-----SSIPRSREDFS--DQVND--- 72
QY 77 LPFSIKYKPIPKISLENVGCASQIGKRNED-----RFDPAQLTDEVLYFA 124
Db 73 -----VSSPRYGVSSVCGRRRREMEADVAIHPSFSPKNSFPQ-----HYFG 114

QY 125 YDGHGCPAAADFCHTHMEKCMDLLPK-----EKNLETLTLTFLAFLDK-----AFS 172
Db 115 YDGHGCHVAARCRERLHKLVQBELSSDMEDEEEMKTTMERSFTRDKVSVNGDSVVT 174

QY 173 SHARLSADATLITS-GTTATVALLRDLGIELVWASVGDSEILCRKPKMLTIDHTPERK 231
Db 175 ANCKDLQTPACDSVGSVAVSVITPD-KIVVANGDSRAVLCKNGKPVFLSDHKDRP 233

QY 232 DEKERIKKCGG-FVWVNSLQPHVNGRLAMTSGIDLDLKTSGVIAPE---TKRIKLH 287
Db 234 DELDRIEAGGRVIYWDG---PRVLGVLAWSRAIGDNLKPY-VSCEPEVTITDR----- 284

QY 288 ADDSFLVLTDTGGINFMVNSQIEICDFVNCQ-----HDP-----NEAAHVAVTEQA 330
Db 285 RDDCLILASDGLWDDVVSNETACSAEMCLRGGRGRQDNEDPAISDKACTEASVLLTKLA 344

R.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayan, L.; Tallon, I.; Reuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A:Reference number: A84420; NUID:20083487; PMID:10617197
A:Accession: D84760
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-239 <STO>
A:Cross-references: GB:AE002093; NID:G3132471; PIDN:AA016260.1; GSPDB:GN00139
C:Genetics:
A:Map position: 2
A:Map position: 2
A:Introns: 48/3; 139/1; 190/3

Query Match 16.5%; Score 322.5; DB 2; Length 239;
Best Local Similarity 34.3%; Pred. No. 9.5e-20;
Matches 81; Conservative 48; Mismatches 80; Indels 27; Gaps 7;

QY 123 FAVYDGHGCPAARDCHTHMEKCIINDLPKKNLETLTLA-FLEIDKAFSHAELSADA 181
DB 20 YAFDGHGSDVADYLNQLH-----FNIILSDPDPWNPKKAKRAYKSTDD 66

QY 182 TLLTS-----GTTATVALLRDGIELVWASVGDSEAILCRKGPMPK-LTIDHTPERKDEK 234
DB 67 YLQNVGPRGSTAVTAIVDGKIVANVWASVGDSEAILCRSDVYKQITVDHEPDK--ER 124

QY 235 ERIKKGCGFVANSIGQPHVNGRLAMTRISIGDLKTS-GVIAEPETKRIKLHADDSEFL 293
DB 125 DLVKGKGFVSQKPGNVRVDQLAMTRAFSGDGLKEHISVIPNTEIAEI---HDDTKFL 181

QY 294 VLTDTGTFMNSQELCPVNOCHPDNEAAHAAVTEQATQYGTEDNSTAVVFPFGAW 349
DB 182 ILASDGLWKNVNDVWDQIKRGNAERAKMLIDKALARGSKDDISCVVVSFLQW 237

RESULT 11
T48123
hypothetical protein F16M2.190 - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T48123
R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, M. submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24459
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-816 <RIE>
A:Cross-references: EMBL:AL139648
A:Experimental source: cultivar Columbia; BAC clone F16M2
C:Genetics:
A:Map position: 3
A:Introns: 4/1; 74/1; 162/2; 197/3; 245/1; 332/2; 454/1; 480/3; 526/1; 578/2; 639/3; 772/2
A:Note: F16M2.190

Query Match 16.5%; Score 322.5; DB 2; Length 816;
Best Local Similarity 27.5%; Pred. No. 5.1e-19;
Matches 112; Conservative 47; Mismatches 100; Indels 149; Gaps 14;

QY 79 PSIKYKPKPKSLNVG-----CASQIGKKEKNE-----REFDFAQLT-- 117
DB 19 PAVFQSPKCPFWLQNWGSPTHSGACRCHTAATQGRNRYQEDRLCALDLRPPPKTKGT 78

QY 118 -DEVL--YFAYVDGHGCPAAADFC-----
DB 79 PKDLVGLIAAVFDGHGAEASDMASKLLDLYPALHINFLDATFSAMTKLIGRFPPTKGD 138

QY 139 -----HTHMEKCI-----DLPKKNLETLTLAFLFIDKAFSS 173
DB 139 HSVILHGVSRDEIMHLYNLDFOQPRDSPLPHFDPSLPLDIMKALLR-AIHDDIVTFTK 197

QY 174 HAEISADATLLTSGTTATVALLRDGIELVWASVGDSEAILC----- 214
DB 198 -----EASNRKLSGSTATIALIADG-OLMVASIGDSKALLCSKFTLEEARATLVKLYR 252

QY 215 -----RKGKPMK-----LTIDHTPERKDEKRIKKGCGFVA-WNSL 249
DB 253 ERRNRGSSPSRSDFKLEHGNLRLFAIAKELTKDHPNREDEKIRVEAAGGVTEM--A 310

QY 250 GQPHVNGRLAMTRISIGDLKTS-GVIAEPETKRIKLHADDSEFLVLTDTGTFMNSQEI 309
DB 311 GVPVNGQLTVSRAIGDLTVRSYGVISAPEVMDWQPLVANDSEFLVSSDGIPEKLEQVEV 370

QY 310 CDFVNOCHDNEA-----AHAVTEQAIQYGTEDNSTAVVVP 345
DB 371 CDLLWEVNNQTSAGAGVPSYCSISLADCLVNTAFKSGMDNMAVVVP 418

RESULT 12
P96752
protein phosphatase 2C (At2P2C-HA), 19519-17666 [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: P96752
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A86141; NUID:21016719; PMID:11130712
A:Accession: P96752
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-511 <STO>
A:Cross-references: GB:AE005173; NID:G6648151; PIDN:AAF21151.1; GSPDB:GN00141
C:Genetics:
A:Gene: F28P22.4
A:Map position: 1

Query Match 16.5%; Score 322; DB 2; Length 511;
Best Local Similarity 30.8%; Pred. No. 2.9e-19;
Matches 100; Conservative 49; Mismatches 102; Indels 74; Gaps 12;

QY 96 GCASQIGKKEKNEEDRF-----DFAQLTDEVL-----YFAYVDGHGCPAA 134
DB 191 GTVSIQGNRSEMEDAFVSPHFLKLPKMLMGDHGMSPLSLTHTGHFFGVYDGHGKHV 250

QY 135 ADPCHTHEKCIIMDLLPKKN-----LETILTAFLEIDKAF----- 171
DB 251 ADYCDRLHFALEAEBIERIKDELCKRNTGEGRQVQWQDKFTSCFLTVDGIEGKIGRAVV 310

QY 172 -SSHARLSADATLLTSGTTATVALLRDGIELVWASVGDSEAILCRKGPMPKLTIDHTPER 230
DB 311 GSDPKVLEAVS-ETVGSTAVVALVCS--HIVSNCGDSRAVLFRGKEMPLSDVHAKPDR 368

QY 231 KDEKERIKKCGG-FVAVNSIGQPHVNGRLAMTRISIGDLKTS-GVIAEPETKRIKLHAD 289
DB 369 EDEVARIENAGGKVIQWGG--ARVFGVLAWSRSIGDRYLPKY-VIPEVTFMP-RSRE 423

QY 290 DSFLVLTDTGTFMNSQEI CDFVNO-----CHDPN-----EAAHAYTE 328
DB 424 DECILIASDGLWDVNNQVECTARRRILMMHKKNGAPPLAERGGKIDPACQAAADYLSM 483

QY 329 QAIQYGTEDNSTAVVVPFGAWKVK 353
DB 484 LALQXGSKDNISIIVIDIKAKQKFK 508

RESULT 13

A56058
phosphoprotein phosphatase (EC 3.1.3.16) 2C - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 18-Feb-2000
C:Accession: A56058; T41353; T38827
R:Shiozaki, K.; Akiyama-Niaki, H.; McGowan, C.H.; Russell, P.
Mol. Cell. Biol. 14, 3742-3751, 1994
A:Title: Protein phosphatase 2C, encoded by ptc1(+), is important in the heat shock resp
A:Reference number: A56058; MUID:94254832; PMID:8196617
A:Accession: A56058
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-347 <SH>
A:Cross-references: GB:126970; NID:9497784; PID:AAA3327.1; PID:9497785
A:Note: authors translated the codon GAT for residue 51 as Asn
A:Note: in the authors' translation residues 51-60 are shown after residue 80, and resid
R:Barrell, B.G.; Rajandream, M.A.; Quail, M.; Harris, D.; Lyne, M.
submitted to the EMBL Data Library, June 1999
A:Reference number: 221814
A:Accession: T41353
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-347 <BA2>
A:Cross-references: EMBL:AL117389; PID:CAB55768.1; GSPDB:GN00068; SPDB:SPCC4F11.02
A:Experimental source: strain 972h-; cosmid c4F11
C:Genetics:
A:Gene: ptc1; SPAC4F11.02
A:Map position: 3
C:Keywords: magnesium; phosphoric monoester hydrolase

Query Match 16.5%; Score 321.5; DB 2; Length 347;
Best Local Similarity 28.8%; Pred. No. 1.9e-19;
Matches 98; Conservative 56; Mismatches 135; Indels 51; Gaps 11;

Qy 27 LQDDRVTPTCHSTSEPCSPDPGSGSPATWNGIWNDRIDEPILLPSIKYKRP 96
Db 11 LLEPHKLNPFSNSTGHRKNASDHSADGE-----TRPIAIEKDKSGNT 56

Qy 87 IP-----KISLNVCSAQIGK--RKENEDR----FDPAQLTDEVLYFAVVDGHHGPA 133
Db 57 VPVGNSPRSKASNLWAGLMEDKQWRWRSMEDTHICLYDFGQNDG--FVAVVDGHHGATQ 115

Qy 134 AADFCHTHMEKCNMLLPKRN--LETLTLTFLAFLDK--AFSSHARLSADAFLLTSGTT 189
Db 116 ASDYCKQNLKLVLEKVRNPDRLVTLMDTEFVNSKIATKATHDI-----CGCT 167

Qy 190 ATVALL-----RGIELAVASVGSRAILCRKPKKLTIDHTPERKDKRIKCKGFFV 244
Db 168 AAVAFRYEKNRTRRVLYTANAGARIVLCRDGRALRLSYDHKGSANESRRVQTGGGLM 227

Qy 245 AMNSLGPHVNGRLAMTRISGDLTKTSGLVIAETPKRIKLHADDSPFLVLTDDGTFNFW 304
Db 228 VQN-----RINGVLAVTRALGDVLYKEL--VSAHPFTTETRIWNGHDEFFIACDGLWDVV 281

Qy 305 NSQEICDFVQCHDNPAAHVAHTEQALQYGTEDNSTAVVV 344
Db 282 SDQEAVDVFRNFSVPREAAVRLVEFALKRLSTDNITCIIV 321

RESULT 14
H84543
Probable protein phosphatase 2C [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 15-Jun-2001
C:Accession: H84543
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.L.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: H84543
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-355 <STO>
A:Cross-references: GB:AEC02093; NID:54559345; PIDN:AAD23006.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g25070
A:Map position: 2
C:Superfamily: human phosphoprotein phosphatase 1A

Query Match 16.4%; Score 320; DB 2; Length 355;
Best Local Similarity 30.8%; Pred. No. 2.7e-19;
Matches 96; Conservative 44; Mismatches 104; Indels 68; Gaps 9;

Qy 96 GCASQIGKRNED--RDFPAQLTDEVLYFAVVDGHHGPAADFCHTHMEKCNMLLPKE 153
Db 25 GLSSNQGWRYATMEHAAILDLDDKTFFGYVDGHHGKVAKFCAYLHQOVSNEAYKT 84

Qy 154 KNLETLTLTFLAFLDK--KAFSSHARLS-----KAFSSHARLS----- 178
Db 85 GDVETSLRRAFRVDDNMQGGWRGLAVLGDKNKFTSGMIEGFIWSPRSGDTNNQPDW 144

Qy 179 -----ADATLLTSGTTATVALLRDGIELVAVSGDSRAILCRKPKMLTIDHTPERK 231
Db 145 PLEDGPHSDFTGPTSGCTACVALIKDK--KLFVANAGDSRCVISRKSQAYNLKDKHDPDL 203

Qy 232 DEKERIKKCGGFVAVNSLQGPVHNGRLAMTRISGDLTKTS-----VIAPETPKRI 283
Db 204 VEKERILKAGGFI-----HAGRINGSNLNTRALGDMFEFKQKFLPSEKQWVADPDINTI 258

Qy 284 KLHADDSPFLVLTDDGTFNFWNSQEI CDVFNQCHDNPAAHVAHTEQALQYGT----- 336
Db 259 DLCD--DDDFLVVACDGIWDCMSQELVDFIHEQLKSETKLSTVCEKVVDRCLAPDTATGE 317

Qy 337 --DNSTAVVVPF 346
Db 318 GCDNNTIILVQF 329

RESULT 15
T05095
hypothetical protein F28M20.60 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Jun-2001
C:Accession: T05095
R:Bevan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Hoheisel, J.; Mewes, F.
submitted to the Protein Sequence Database, November 1998
A:Reference number: 215398
A:Accession: T05095
A:Molecule type: DNA
A:Residues: 1-389 <BEV>
A:Cross-references: EMBL:AL031004
A:Experimental source: cultivar Columbia; BAC clone F28M20
C:Genetics:
A:Map position: 4
A:Introns: 95/1; 128/1; 181/1; 210/1; 274/3; 318/3
A:Note: F28M20.60
C:Superfamily: human phosphoprotein phosphatase 1A

Query Match 16.4%; Score 319.5; DB 2; Length 389;
Best Local Similarity 30.8%; Pred. No. 3.3e-19;
Matches 97; Conservative 45; Mismatches 92; Indels 81; Gaps 11;

Qy 96 GCASQIGKRNED--RDFPAQLTDEVLYFAVVDGHHGPAADFCHTHMEKCNMLLP 151
Db 60 GYASPGKRSMEFYETRIDGVE--GEIVGLFGVDFGHHGARAAYVKQNL---FSLIR 115

Qy 152 KEKQLETLTLTFLAFLDKAFSSHARLSADAFLLTS-----GTTATVALLRDGIELVV 203
Db 116 HPK-----FISDITAAIADAVNTDSEFLKSENSQNRDAGSTASTAIL--VGDELLV 165

Qy 204 ASVGDRAILCRKPKMLTIDHTPERKDKERIKKCGGFVAVNSLQGPVHNGRLAMTRIS 263
Db 166 ANVGDSRAVICRGNAIVASRDHKPDQSDERQRIEDAGGFVW--AGTWVGGVLAVSRA 223

QY	264	IGDLDLKTSGVIAEPE-----TKRIKLH-----	287
Db	224	FGRLRK-QYVADPEIQVLTFCQNLILYIKNATLLTIEHNLHWISIVSYINGTLQNFL	282
QY	288	-----ADDS--FLVLTDDGINFVNVSQEICDFVNOCHDPNEAAHAYTEQAI	331
Db	283	RSLISINGKFOEEKVDSSLEFLILASDGLWDVVSNEEAVGMIKATEDPEGAKRLMMEAY	342
QY	332	QYGTEDNSTAVVVPF	346
Db	343	QGSADNITCVVVR	357

Search completed: October 12, 2004, 05:58:49
 Job time : 39 secs

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